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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds
(without alignments)
71.766 Million cell updates/sec

Title: US-09-787-443A-1
Perfect score: 11
Sequence: 1 ASKKPKRNIKA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11	100.0	11	3	AAy88527	Aay88527 NCAM Ig1
2	11	100.0	11	5	ABg69329	Abg69329 Human neu
3	6	54.5	11	3	AAy88553	Aay88553 NCAM Ig1
4	6	54.5	11	3	AAy88557	Aay88557 NCAM Ig1
5	5	45.5	11	3	AAy88554	Aay88554 NCAM Ig1
6	4	36.4	11	2	AAw53153	Aaw53153 PTP activ
7	4	36.4	11	3	AAy88556	Aay88556 NCAM Ig1
8	4	36.4	11	3	AAy88555	Aay88555 NCAM Ig1
9	4	36.4	11	5	ABB74833	Abb74833 Nuclear p

10	3	27.3	11	1	AAP50268	Aap50268	Yeast alp
11	3	27.3	11	2	AAR27765	Aar27765	BSA-bind
12	3	27.3	11	2	AAR30814	Aar30814	Humanised
13	3	27.3	11	2	AAR34247	Aar34247	Mutant HT
14	3	27.3	11	2	AAR34252	Aar34252	Mutant HT
15	3	27.3	11	2	AAR34255	Aar34255	Mutant HT
16	3	27.3	11	2	AAR34257	Aar34257	Mutant HT
17	3	27.3	11	2	AAR34256	Aar34256	Mutant HT
18	3	27.3	11	2	AAR34254	Aar34254	Mutant HT
19	3	27.3	11	2	AAR34248	Aar34248	Mutant HT
20	3	27.3	11	2	AAR34253	Aar34253	Mutant HT
21	3	27.3	11	2	AAR34246	Aar34246	HTLV-I re
22	3	27.3	11	2	AAR49995	Aar49995	Mouse OSF
23	3	27.3	11	2	AAR67121	Aar67121	Factor V
24	3	27.3	11	2	AAR70367	Aar70367	Borrelia
25	3	27.3	11	2	AAR52710	Aar52710	Enkephali
26	3	27.3	11	2	AAW06227	Aaw06227	LHRH anta
27	3	27.3	11	2	AAW06228	Aaw06228	LHRH anta
28	3	27.3	11	2	AAR68911	Aar68911	Factor-VI
29	3	27.3	11	2	AAR67858	Aar67858	FVII/TF m
30	3	27.3	11	2	AAW21329	Aaw21329	Glucagon
31	3	27.3	11	2	AAW21466	Aaw21466	Islet amy
32	3	27.3	11	2	AAW21467	Aaw21467	Islet amy
33	3	27.3	11	2	AAR84537	Aar84537	Hepatitis
34	3	27.3	11	2	AAR67274	Aar67274	Synthetic
35	3	27.3	11	2	AAR99265	Aar99265	Myosin li
36	3	27.3	11	2	AAW05350	Aaw05350	Residues
37	3	27.3	11	2	AAR92022	Aar92022	Multiple
38	3	27.3	11	2	AAW41825	Aaw41825	Modified
39	3	27.3	11	2	AAW10458	Aaw10458	Human gro
40	3	27.3	11	2	AAW10460	Aaw10460	Human gro
41	3	27.3	11	2	AAW33181	Aaw33181	Mono-DTPA
42	3	27.3	11	2	AAW23266	Aaw23266	Tumour ne
43	3	27.3	11	2	AAW39588	Aaw39588	Human mel
44	3	27.3	11	2	AAW09910	Aaw09910	Prostate
45	3	27.3	11	2	AAY22688	Aay22688	Neurokini
46	3	27.3	11	2	AAW10197	Aaw10197	Serum imm
47	3	27.3	11	2	AAW18223	Aaw18223	Mycobacte
48	3	27.3	11	2	AAW10140	Aaw10140	Hepatitis
49	3	27.3	11	2	AAW35543	Aaw35543	Immunizat
50	3	27.3	11	2	AAW12550	Aaw12550	Japanese
51	3	27.3	11	2	AAW39795	Aaw39795	Tobacco P
52	3	27.3	11	2	AAW62014	Aaw62014	Light cha
53	3	27.3	11	2	AAY20193	Aay20193	Human bet
54	3	27.3	11	2	AAW78614	Aaw78614	SH2 domai
55	3	27.3	11	2	AAW62443	Aaw62443	Human neu
56	3	27.3	11	2	AAW79785	Aaw79785	Amino aci
57	3	27.3	11	2	AAW84064	Aaw84064	Human V3
58	3	27.3	11	2	AAY03664	Aay03664	Amino aci
59	3	27.3	11	2	AAY42674	Aay42674	HHV-6 var
60	3	27.3	11	3	AAY81921	Aay81921	Asparagin
61	3	27.3	11	3	AAY82340	Aay82340	Humanised
62	3	27.3	11	3	AAY85087	Aay85087	HBV surfa
63	3	27.3	11	3	AAY88529	Aay88529	NCAM Igl
64	3	27.3	11	3	AAY88563	Aay88563	NCAM Igl
65	3	27.3	11	3	AAY88560	Aay88560	NCAM Igl
66	3	27.3	11	3	AAY88538	Aay88538	NCAM Igl

67	3	27.3	11	3	AAy99060	Aay99060	HLA class
68	3	27.3	11	3	AAy78451	Aay78451	Human gro
69	3	27.3	11	3	AAy78449	Aay78449	Human gro
70	3	27.3	11	3	AAy90160	Aay90160	UPAR targ
71	3	27.3	11	3	AAy87899	Aay87899	M. tuberc
72	3	27.3	11	3	AAy81884	Aay81884	Yeast SAH
73	3	27.3	11	3	AAB35570	Aab35570	Uteroglob
74	3	27.3	11	3	AAB35573	Aab35573	Uteroglob
75	3	27.3	11	4	AAM97950	Aam97950	Human pep
76	3	27.3	11	4	AAM97944	Aam97944	Human pep
77	3	27.3	11	4	AAM99160	Aam99160	Vaccine r
78	3	27.3	11	4	AAB84910	Aab84910	Peptide f
79	3	27.3	11	4	AAB92043	Aab92043	Growth fa
80	3	27.3	11	4	AAE09385	Aae09385	Human her
81	3	27.3	11	4	AAU24973	Aau24973	Schizophr
82	3	27.3	11	4	AAB67064	Aab67064	Recombina
83	3	27.3	11	4	AAU09909	Aau09909	Rat mAb Y
84	3	27.3	11	4	AAU27153	Aau27153	Human Leu
85	3	27.3	11	4	AAU26843	Aau26843	Human Leu
86	3	27.3	11	4	AAE05947	Aae05947	Basic ami
87	3	27.3	11	4	AAE12225	Aae12225	Mycobacte
88	3	27.3	11	4	AAB64173	Aab64173	Human Cla
89	3	27.3	11	4	AAB64170	Aab64170	Human Cla
90	3	27.3	11	4	ABP13080	Abp13080	HIV A02 s
91	3	27.3	11	4	ABP13796	Abp13796	HIV A02 s
92	3	27.3	11	4	ABP14147	Abp14147	HIV A02 s
93	3	27.3	11	4	ABP20760	Abp20760	HIV A03 m
94	3	27.3	11	4	ABP20751	Abp20751	HIV A03 m
95	3	27.3	11	4	ABP23008	Abp23008	HIV A11 m
96	3	27.3	11	4	ABP14880	Abp14880	HIV A03 s
97	3	27.3	11	4	ABP19004	Abp19004	HIV B62 s
98	3	27.3	11	4	ABP19475	Abp19475	HIV B62 s
99	3	27.3	11	4	ABP14625	Abp14625	HIV A03 s
100	3	27.3	11	4	ABP16896	Abp16896	HIV B07 s

ALIGNMENTS

RESULT 1

AAy88527

ID AAY88527 standard; peptide; 11 AA.

XX

AC AAY88527;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide C3.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-DK000500.
XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.
XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX
DR WPI; 2000-293111/25.
XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.
XX
PS Claim 20; Page 82; 119pp; English.
XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASKKPKRNIKA 11
| | | | | | | | | |
Db 1 ASKKPKRNIKA 11

RESULT 2

ABG69329

ID ABG69329 standard; peptide; 11 AA.

XX

AC ABG69329;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #1.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,
PT in the preparation of medicament for preventing death of cells presenting
PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Claim 26; Page 39; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which
CC comprises at least 5 contiguous amino acid residues of a sequence of the
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,
CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
 CC of a medicament for preventing death of cells presenting the NCAM or an
 CC NCAM ligand. The medicament is for the stimulation of the survival of
 CC heart muscle cells, such as survival after acute myocardial infarction.
 CC The medicament is for the treatment of diseases or conditions of the
 CC central and peripheral nervous system, such as postoperative nerve
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
 CC impaired myelination of nerve fibres, postischaemic damage, e.g.
 CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
 CC degeneration associated with diabetes mellitus, neuro-muscular
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
 CC Huntington's disease. The medicament is for the treatment of diseases or
 CC conditions of the muscles including conditions with impaired function of
 CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
 CC disorders, and for the treatment of diseases or conditions of various
 CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
 CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
 CC ABG69352 represent human NCAM peptides of the invention
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASKKPKRNIKA 11
 |||||
 Db 1 ASKKPKRNIKA 11

RESULT 3

AAY88553

ID AAY88553 standard; peptide; 11 AA.

XX

AC AAY88553;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide 116 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.

XX

PS Example 5; Fig 7; 119pp; English.

XX

CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The invention relates to a compound containing a peptide which
CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,
CC and is capable of stimulating or promoting neurite outgrowth from NCAM
CC presenting cells, and is also capable of promoting the proliferation of
CC NCAM presenting cells. The present sequence represents a control peptide
CC used in the identification of those binding peptides which can be used in
CC the compound. The compound may be used in the treatment of normal,
CC degenerated or damaged NCAM presenting cells. The compound may in
CC particular be used to treat diseases of the central and peripheral
CC nervous systems such as post operative nerve damage, traumatic nerve
CC damage, impaired myelination of nerve fibres, conditions resulting from a
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
CC nerve degeneration associated with diabetes mellitus, disorders affecting
CC the circadian clock or neuro-muscular transmission and schizophrenia.
CC Conditions affecting the muscles may also be treated with the compound,
CC such as conditions associated with impaired function of neuromuscular
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
CC be treated using the compound. The compound is used in a prosthetic nerve
CC guide, and also to stimulate the ability to learn, and to stimulate the
CC memory of a subject

XX

SQ Sequence 11 AA;

Query Match 54.5%; Score 6; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 ASKKPK 6

Db 111111
 1 ASKKPK 6

RESULT 4

AAAY88557

ID AAAY88557 standard; peptide; 11 AA.

XX

AC AAAY88557;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide 120 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.

XX

PS Example 5; Fig 7; 119pp; English.

XX

CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
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CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin

CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The invention relates to a compound containing a peptide which
CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,
CC and is capable of stimulating or promoting neurite outgrowth from NCAM
CC presenting cells, and is also capable of promoting the proliferation of
CC NCAM presenting cells. The present sequence represents a control peptide
CC used in the identification of those binding peptides which can be used in
CC the compound. The compound may be used in the treatment of normal,
CC degenerated or damaged NCAM presenting cells. The compound may in
CC particular be used to treat diseases of the central and peripheral
CC nervous systems such as post operative nerve damage, traumatic nerve
CC damage, impaired myelination of nerve fibres, conditions resulting from a
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
CC nerve degeneration associated with diabetes mellitus, disorders affecting
CC the circadian clock or neuro-muscular transmission and schizophrenia.
CC Conditions affecting the muscles may also be treated with the compound,
CC such as conditions associated with impaired function of neuromuscular
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
CC be treated using the compound. The compound is used in a prosthetic nerve
CC guide, and also to stimulate the ability to learn, and to stimulate the
CC memory of a subject

XX

SQ Sequence 11 AA;

Query Match 54.5%; Score 6; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRNIKA 11
| | | | |
Db 6 KRNIKA 11

RESULT 5

AA88554

ID AA88554 standard; peptide; 11 AA.

XX

AC AA88554;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Ig1 binding peptide 117 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.

XX

PS Example 5; Fig 7; 119pp; English.

XX

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CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The invention relates to a compound containing a peptide which
CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,
CC and is capable of stimulating or promoting neurite outgrowth from NCAM
CC presenting cells, and is also capable of promoting the proliferation of
CC NCAM presenting cells. The present sequence represents a control peptide
CC used in the identification of those binding peptides which can be used in
CC the compound. The compound may be used in the treatment of normal,
CC degenerated or damaged NCAM presenting cells. The compound may in
CC particular be used to treat diseases of the central and peripheral
CC nervous systems such as post operative nerve damage, traumatic nerve
CC damage, impaired myelination of nerve fibres, conditions resulting from a
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
CC nerve degeneration associated with diabetes mellitus, disorders affecting
CC the circadian clock or neuro-muscular transmission and schizophrenia.
CC Conditions affecting the muscles may also be treated with the compound,
CC such as conditions associated with impaired function of neuromuscular
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
CC be treated using the compound. The compound is used in a prosthetic nerve
CC guide, and also to stimulate the ability to learn, and to stimulate the
CC memory of a subject

XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASKKP 5
| | | | |
Db 1 ASKKP 5

RESULT 6

AAW53153

ID AAW53153 standard; peptide; 11 AA.

XX

AC AAW53153;

XX

DT 14-JUL-1998 (first entry)

XX

DE PTP activity determining peptide substrate 8.

XX

KW Protein tyrosine phosphatase; PTP; peptide substrate; phosphorylation.

XX

OS Synthetic.

XX

PN US5739278-A.

XX

PD 14-APR-1998.

XX

PF 30-MAR-1995; 95US-00416035.

XX

PR 10-MAY-1993; 93US-00059949.

XX

PA (UNIW) UNIV WASHINGTON.

XX

PI Fischer EH, Cool DE, Daum G;

XX

DR WPI; 1998-250491/22.

XX

PT New nona-peptide, phosphorylated derivative and related compositions -
PT useful for measuring activity of protein tyrosine phosphatases.

XX

PS Disclosure; Col 13-14; 5pp; English.

XX

CC This peptide substrate can be used for the determination of activity of
CC protein tyrosine phosphatases (PTP). The peptides with a tyrosine residue
CC phosphorylated and related compositions containing the peptides are
CC useful for determining the amount or presence of PTP. Determination of
CC PTP activity by prior art methods could be affected by a number of
CC factors, including the type of enzyme being assayed, the conditions under
CC which the assay was performed and the presence of external effectors. The
CC peptide of the current invention, when used as a substrate for
CC determination purposes is not subject to the limitations of prior art
CC methods. The new determination method is highly sensitive, with the assay
CC permitting the detection and characterisation of a wide variety of PTP's.
CC Due to the increased sensitivity of the methods, PTP's can be detected in
CC situations where only limiting amounts of samples, e.g tissue extracts or
CC immunoprecipitates, are available

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASKK 4
||||
Db 7 ASKK 10

RESULT 7

AAY88556

ID AAY88556 standard; peptide; 11 AA.

XX

AC AAY88556;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Ig1 binding peptide 119 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating

PT disorders of the nervous system and muscles e.g. Alzheimer's and

PT Parkinson's diseases.

XX
PS Example 5; Fig 7; 119pp; English.
XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The invention relates to a compound containing a peptide which
CC binds to the NCAM Igl domain. The compound binds to NCAM-Igl/Ig2 domains,
CC and is capable of stimulating or promoting neurite outgrowth from NCAM
CC presenting cells, and is also capable of promoting the proliferation of
CC NCAM presenting cells. The present sequence represents a control peptide
CC used in the identification of those binding peptides which can be used in
CC the compound. The compound may be used in the treatment of normal,
CC degenerated or damaged NCAM presenting cells. The compound may in
CC particular be used to treat diseases of the central and peripheral
CC nervous systems such as post operative nerve damage, traumatic nerve
CC damage, impaired myelination of nerve fibres, conditions resulting from a
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
CC nerve degeneration associated with diabetes mellitus, disorders affecting
CC the circadian clock or neuro-muscular transmission and schizophrenia.
CC Conditions affecting the muscles may also be treated with the compound,
CC such as conditions associated with impaired function of neuromuscular
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
CC be treated using the compound. The compound is used in a prosthetic nerve
CC guide, and also to stimulate the ability to learn, and to stimulate the
CC memory of a subject
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIKA 11
| | | |
Db 8 NIKA 11

RESULT 8

AAAY88555

ID AAY88555 standard; peptide; 11 AA.

XX

AC AAY88555;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide 118 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX
 OS Synthetic.
 XX
 PN WO200018801-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 23-SEP-1999; 99WO-DK000500.
 XX
 PR 29-SEP-1998; 98DK-00001232.
 PR 29-APR-1999; 99DK-00000592.
 XX
 PA (RONN/) RONN L C B.
 PA (BOCK/) BOCK E.
 PA (HOLM/) HOLM A.
 PA (OLSE/) OLSEN M.
 PA (OSTE/) OSTERGAARD S.
 PA (JENS/) JENSEN P H.
 PA (POUL/) POULSEN F M.
 PA (SORO/) SOROKA V.
 PA (RALE/) RALETS I.
 PA (BERE/) BEREZIN V.
 XX
 PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;
 XX
 DR WPI; 2000-293111/25.
 XX
 PT Compositions that bind neural cell adhesion molecules useful for treating
 PT disorders of the nervous system and muscles e.g. Alzheimer's and
 PT Parkinson's diseases.
 XX
 PS Example 5; Fig 7; 119pp; English.
 XX
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
 CC NCAM is found in three forms, two of which are transmembrane forms, while
 CC the third is attached via a lipid anchor to the cell membrane. All three
 CC NCAM forms have an extracellular structure consisting five immunoglobulin
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
 CC terminal. The invention relates to a compound containing a peptide which
 CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,
 CC and is capable of stimulating or promoting neurite outgrowth from NCAM
 CC presenting cells, and is also capable of promoting the proliferation of
 CC NCAM presenting cells. The present sequence represents a control peptide
 CC used in the identification of those binding peptides which can be used in
 CC the compound. The compound may be used in the treatment of normal,
 CC degenerated or damaged NCAM presenting cells. The compound may in
 CC particular be used to treat diseases of the central and peripheral
 CC nervous systems such as post operative nerve damage, traumatic nerve
 CC damage, impaired myelination of nerve fibres, conditions resulting from a
 CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
 CC nerve degeneration associated with diabetes mellitus, disorders affecting
 CC the circadian clock or neuro-muscular transmission and schizophrenia.
 CC Conditions affecting the muscles may also be treated with the compound,
 CC such as conditions associated with impaired function of neuromuscular
 CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
 CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus

CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
CC be treated using the compound. The compound is used in a prosthetic nerve
CC guide, and also to stimulate the ability to learn, and to stimulate the
CC memory of a subject
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIKA 11
 ||||
Db 8 NIKA 11

RESULT 9
ABB74833

ID ABB74833 standard; peptide; 11 AA.
XX
AC ABB74833;
XX
DT 18-APR-2002 (first entry)
XX
DE Nuclear protein nuclear localisation signal peptide SEQ ID NO:597.
XX
KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.
XX
OS Parechinus angulosus.
XX
PN WO200193836-A2.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US018657.
XX
PR 09-JUN-2000; 2000US-0210925P.
XX
PA (BOUL/) BOULIKAS T.
XX
PI Boulikas T;
XX
DR WPI; 2002-164295/21.
XX
PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.
XX
PS Claim 14; Page 85; 107pp; English.
XX
CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on

CC lipid molecules to form an electrostatic micelle complex in 20-80 %
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
 CC micelles with entrapped therapeutic agents. Also described is a method
 CC for delivering a therapeutic agent in vivo, comprising the administration
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
 CC nuclear localisation signal (NLS) peptides for use in the method as the
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
 CC and antitumour activities. The peptide-lipid-polynucleotide complexes
 CC produced are useful for inhibiting the progression of neoplastic
 CC diseases. The invention relates to the field of gene therapy and is
 CC directed toward methods for producing peptide-lipid-polynucleotide
 CC complexes suitable for delivery of polynucleotides. The encapsulated
 CC molecules display therapeutic efficacy in eradicating solid tumours
 CC including but not limited to breast carcinoma or prostate carcinoma.
 CC ABB74235 to ABB74255 are used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKPK 6
 ||||
 Db 5 KKPK 8

RESULT 10
 AAP50268

ID AAP50268 standard; protein; 11 AA.

XX

AC AAP50268;

XX

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 26-NOV-1991 (first entry)

XX

DE Yeast alpha-factor secretory leader linked to N-terminal human epidermal
 DE growth factor.

XX

KW Epidermal growth factor; alpha-factor secretory leader; yeast;

KW DNA construct; plasmid pY alpha EGF-24.

XX

OS Saccharomyces cerevisiae.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .7

FT /label= alpha-factor secretory leader

FT Region 8. .12

FT /label= human epidermal growth factor N-terminal

XX

PN W08502200-A.

XX

PD 23-MAY-1985.

XX
 PF 09-NOV-1984; 84WO-US001853.
 XX
 PR 14-NOV-1983; 83US-00551443.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Barr P, Merryweath JP;
 XX
 DR WPI; 1985-134837/22.
 DR N-PSDB; AAN50323.
 XX
 PT DNA construct encoding human interleukin-2 gene - useful in transformed
 PT microorganism for expressing the polypeptide.
 XX
 PS Disclosure; Page 15; 3lpp; English.
 XX
 CC The peptide is encoded by a DNA which was obtd. by in vitro mutagenesis
 CC of the DNA of AAN50320, which was a modification of the DNA from clone
 CC pYEGF-8 (in which the region corresp. to bacterial plasmid pMB9 in
 CC pJDB219 has been replaced by pBR322 in pC1/1). It comprises the joining
 CC of the N-terminal of the human epidermal growth factor structural gene to
 CC the yeast alpha-factor secretory leader sequence, thus providing for
 CC different processing signals. In the present DNA, the dipeptidyl
 CC aminopeptidase maturation site (Glu-Ala) has been removed. The resulting
 CC yeast plasmid is named pY alpha EGF-24. The DNA contains a new KpnI site.
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
 |||
 Db 6 KRN 8

RESULT 11

AAR27765

ID AAR27765 standard; peptide; 11 AA.

XX

AC AAR27765;

XX

DT 25-MAR-2003 (revised)

DT 03-MAR-1993 (first entry)

XX

DE BSA-binding disulphide-constrained micropeptide #1.

XX

KW Potential binding domain; TN2 phage library; bovine serum albumen.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 4. .9

XX
 PN WO9215677-A1.
 XX
 PD 17-SEP-1992.
 XX
 PF 27-FEB-1992; 92WO-US001456.
 XX
 PR 01-MAR-1991; 91US-00664989.
 XX
 PA (PROT-) PROTEIN ENG CORP.
 XX
 PI Ladner RC, Roberts BL, Ley AC, Kent RB;
 XX
 DR WPI; 1992-331723/40.
 XX
 PT Developing binding proteins for target material - using library
 PT displaying chimeric micro-proteins having intra-chain covalent crosslink.
 XX
 PS Example 1; Page 123; 151pp; English.
 XX
 CC DNA coding for a family of microproteins containing a cystine moiety with
 CC a disulphide bridge span of 4 amino acids was fused to the gene III of
 CC M13. The fusion proteins were displayed on the phage surface. The library
 CC was screened for streptavidin binding micropeptides; the phage were bound
 CC to bovine serum albumen-coated wells and bound phage were eluted and used
 CC to infect bacteria. New phage stock was harvested for two further
 CC enhancement cycles, after which some of the individual phage were
 CC sequenced and tested. Micropeptide #1 is one of the peptide sequences
 CC which bound to BSA; there was no consensus motif between the cysteine
 CC residues of the 8 micropeptides isolated by this procedure. See also
 CC AAR27766-R27772. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
 |||
 Db 6 KRN 8

RESULT 12
 AAR30814

ID AAR30814 standard; protein; 11 AA.

XX

AC AAR30814;

XX

DT 25-MAR-2003 (revised)

DT 08-JUN-1993 (first entry)

XX

DE Humanised antibody light chain CDR 1.

XX

KW Complementarity determining region; CDR; rat; monoclonal; antibody;

KW YFC51.1.1; CD18; humanised; antigen; leukocyte; lung; sepsis; asthma;

KW endotoxic shock; adult respiratory distress syndrome; inflammation;

KW immunotoxin.
 XX
 OS Rattus rattus.
 XX
 PN WO9302191-A1.
 XX
 PD 04-FEB-1993.
 XX
 PF 15-JUL-1992; 92WO-GB001289.
 XX
 PR 16-JUL-1991; 91GB-00015364.
 XX
 PA (WELL) WELLCOME FOUND LTD.
 XX
 PI Waldmann H, Sims M, Crowe S;
 XX
 DR WPI; 1993-058788/07.
 DR N-PSDB; AAQ35171.
 XX
 PT New humanised antibody specific for human CD-18 antigen - inhibits influx
 PT of leukocytes into the lungs, useful for treating endotoxic shock, adult
 PT respiratory distress syndrome, asthma, etc.
 XX
 PS Claim 1; Page 33; 59pp; English.
 XX
 CC The sequences given in AAR30814-16 represent the light chain complement-
 CC arity determining regions (CDRs) of the rat monoclonal antibody YFC51.1.1
 CC (see also AAR30820-21). YFC51.1.1 is a CD18 antibody. These CDRs can be
 CC used in a humanised antibody with specificity for CD18 antigen. The
 CC antibody may be useful in treating leukocyte-mediated conditions, such as
 CC inhibiting influx of leukocytes into the lung and other organs during
 CC sepsis, endotoxic shock or adult respiratory distress syndrome. The
 CC antibodies may also be used to treat asthma and inflammation and may form
 CC part of an immunotoxin. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
 |||
 Db 2 ASK 4

RESULT 13
 AAR34247
 ID AAR34247 standard; peptide; 11 AA.
 XX
 AC AAR34247;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-AUG-1993 (first entry)
 XX
 DE Mutant HTLV-I residues 88-98, peptide 2L-1.1.
 XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
 KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.
 XX
 OS Synthetic.
 XX
 PN WO9306843-A1.
 XX
 PD 15-APR-1993.
 XX
 PF 08-OCT-1992; 92WO-US008405.
 XX
 PR 08-OCT-1991; 91US-00771553.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Palker TJ, Haynes BF;
 XX
 DR WPI; 1993-134125/16.
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
 XX
 PS Example 7; Page 32; 50pp; English.
 XX
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
 |||
 Db 3 KKP 5

RESULT 14

AAR34252

ID AAR34252 standard; peptide; 11 AA.

XX

AC AAR34252;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.6.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;

KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX
 OS Synthetic.
 XX
 PN WO9306843-A1.
 XX
 PD 15-APR-1993.
 XX
 PF 08-OCT-1992; 92WO-US008405.
 XX
 PR 08-OCT-1991; 91US-00771553.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Palker TJ, Haynes BF;
 XX
 DR WPI; 1993-134125/16.
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
 XX
 PS Example 7; Page 32; 50pp; English.
 XX
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
 |||
 Db 3 KKP 5

RESULT 15

AAR34255

ID AAR34255 standard; peptide; 11 AA.

XX

AC AAR34255;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.9.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;

KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX
 PN WO9306843-A1.
 XX
 PD 15-APR-1993.
 XX
 PF 08-OCT-1992; 92WO-US008405.
 XX
 PR 08-OCT-1991; 91US-00771553.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Palker TJ, Haynes BF;
 XX
 DR WPI; 1993-134125/16.
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
 XX
 PS Example 7; Page 32; 50pp; English.
 XX
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
 |||
 Db 3 KKP 5

RESULT 16

AAR34257

ID AAR34257 standard; peptide; 11 AA.

XX

AC AAR34257;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.11.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;

KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX
PD 15-APR-1993.
XX
PF 08-OCT-1992; 92WO-US008405.
XX
PR 08-OCT-1991; 91US-00771553.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Palker TJ, Haynes BF;
XX
DR WPI; 1993-134125/16.
XX
PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
XX
PS Example 7; Page 32; 50pp; English.
XX
CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-56.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
| | |
Db 3 KKP 5

RESULT 17

AAR34256

ID AAR34256 standard; peptide; 11 AA.

XX

AC AAR34256;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.10.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX
 PF 08-OCT-1992; 92WO-US008405.
 XX
 PR 08-OCT-1991; 91US-00771553.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Palker TJ, Haynes BF;
 XX
 DR WPI; 1993-134125/16.
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
 XX
 PS Example 7; Page 32; 50pp; English.
 XX
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
 |||
 Db 3 KKP 5

RESULT 18

AAR34254

ID AAR34254 standard; peptide; 11 AA.

XX

AC AAR34254;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.8.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
 KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX
 PR 08-OCT-1991; 91US-00771553.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Palker TJ, Haynes BF;
 XX
 DR WPI; 1993-134125/16.
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
 XX
 PS Example 7; Page 32; 50pp; English.
 XX
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
 |||
 Db 3 KKP 5

RESULT 19

AAR34248

ID AAR34248 standard; peptide; 11 AA.

XX

AC AAR34248;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.2.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
 KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX
PA (UYDU-) UNIV DUKE.
XX
PI Palker TJ, Haynes BF;
XX
DR WPI; 1993-134125/16.
XX
PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
XX
PS Example 7; Page 32; 50pp; English.
XX
CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 3 KKP 5

RESULT 20

AAR34253

ID AAR34253 standard; peptide; 11 AA.

XX

AC AAR34253;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.7.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX
 PI Palker TJ, Haynes BF;
 XX
 DR WPI; 1993-134125/16.
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
 XX
 PS Example 7; Page 32; 50pp; English.
 XX
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
 |||
 Db 3 KKP 5

RESULT 21

AAR34246

ID AAR34246 standard; peptide; 11 AA.

XX

AC AAR34246;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE HTLV-I residues 88-98, peptide 2L-1.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
 KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX
 DR WPI; 1993-134125/16.
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
 XX
 PS Example 7; Page 32; 50pp; English.
 XX
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
 |||
 Db 3 KKP 5

RESULT 22

AAR49995

ID AAR49995 standard; protein; 11 AA.

XX

AC AAR49995;

XX

DT 25-MAR-2003 (revised)

DT 23-SEP-1994 (first entry)

XX

DE Mouse OSF-5 antigenic peptide 116-126.

XX

KW Mouse OSF-5; bone-related carboxypeptidase-like protein; growth factor;

KW adhesion molecule; osteogenesis; bone induction;

KW bone metabolism disorder; osteoporosis; osteopetrosis; Paget's disease;

KW antigen; immunogen; detection.

XX

OS Synthetic.

XX

PN EP588118-A2.

XX

PD 23-MAR-1994.

XX

PF 25-AUG-1993; 93EP-00113604.

XX

PR 28-AUG-1992; 92JP-00230029.

PR 03-DEC-1992; 92JP-00324033.

XX

PA (FARH) HOECHST JAPAN LTD.

PA (HMRI) HOECHST MARION ROUSSELL LTD.

XX
 PI Kawai S, Takeshita S, Okazaki M, Amann E;
 XX
 DR WPI; 1994-093794/12.
 XX
 PT New bone-related carboxypeptidase OSF-5 - used to obtain prods. for the
 PT diagnosis and treatment of bone metabolic diseases, e.g. osteoporosis, or
 PT Paget's disease.
 XX
 PS Example 5; Page 6; 26pp; English.
 XX
 CC OSF-5 is a bone-specific carboxypeptidase which acts as an adhesion
 CC molecule or growth factor; it takes part in osteogenesis at the site of
 CC bone induction. OSF-5 can be used to treat bone metabolic diseases, e.g.
 CC osteoporosis, Paget's disease, osteomalacia, hyperostosis or
 CC osteopetrosis. To prepare anti-OSF-5 antibodies, five peptides (see
 CC AAR49995-R49999) corresponding to regions of the full-length mouse OSF-5
 CC sequence (AAR49994) were synthesised. Antisera raised against the
 CC peptides could be used to immunohistochemically search for the presence
 CC of OSF-5 in systemic slices from newborn mice and to detect expression of
 CC OSF-5 in E.coli, yeast and animal cells. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
 |||
 Db 1 KPK 3

RESULT 23

AAR67121

ID AAR67121 standard; peptide; 11 AA.

XX

AC AAR67121;

XX

DT 25-MAR-2003 (revised)

DT 30-JUN-1995 (first entry)

XX

DE Factor V derived (AC-5A1) peptide, contg. proline brackets.

XX

KW blood protein inhibitor; antagonist; thrombin; prothrombin; mimic;
 KW interaction site; constrained conformation; inhibitor.

XX

OS Synthetic.

XX

PN WO9425482-A1.

XX

PD 10-NOV-1994.

XX

PF 21-APR-1994; 94WO-US004294.

XX

PR 23-APR-1993; 93US-00051741.

PR 29-OCT-1993; 93US-00143364.

XX

PA (EVAN/) EVANS H J.

PA (KINI/) KINI R M.

XX

PI Evans HJ, Kini RM;

XX

DR WPI; 1994-358186/44.

XX

PT Peptide homologue or analogue with constrained conformation - has proline
PT residues flanking the interaction site to impart greater, or more stable,
PT biological activity.

XX

PS Example 3; Page 39; 57pp; English.

XX

CC AAR67121-39 are blood protein inhibitors and antagonists. The peptides
CC are deriv. from naturally occurring polypeptides that contain proline or
CC proline/cysteine brackets. These peptides contain one or more interaction
CC sites of interest. AAR67121-22 are deriv. from factor V. The dose is 1-2
CC millimoles. The peptides interfere with the generation of thrombin from
CC prothrombin. The data collected demonstrates that interaction sites
CC possess activity when present in a polypeptide that differs from the
CC native form. Inclusion of conformation-constraining moieties can have
CC desirable effects on an interaction site. (Also see AAR67011-120 and
CC AAR67140-52 for analogues of other biologically active peptides contg. an
CC interaction site flanked by conformation constraining gps., eg. RGD
CC peptides.) (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3

|||

Db 4 ASK 6

RESULT 24

AAR70367

ID AAR70367 standard; peptide; 11 AA.

XX

AC AAR70367;

XX

DT 25-MAR-2003 (revised)

DT 25-MAY-1995 (first entry)

XX

DE Borrelia OspC antigen epitope.

XX

KW OspC antigen; vaccine; Lyme disease; borreliosis; immunogen;

KW serovar typing; restriction fragment length polymorphism; RFLP.

XX

OS Borrelia burgdorferi.

XX

PN WO9425596-A2.

XX

PD 10-NOV-1994.
 XX
 PF 29-APR-1994; 94WO-EP001365.
 XX
 PR 29-APR-1993; 93US-00053863.
 XX
 PA (IMMO) IMMUNO AG.
 XX
 PI Livey I, Crowe B, Dorner F;
 XX
 DR WPI; 1994-358273/44.
 XX
 PT Immunogenic composition comprising OspC antigens - for the treatment of
 PT Lyme borreliosis in different, specific geographical areas.
 XX
 PS Claim 19; Page 57; 115pp; English.
 XX
 CC A vaccine for Lyme disease includes selected OspC antigen formulations
 CC based on defined OspC families resolved by serovar typing and RFLP typing
 CC of strains of worldwide origin. The antigens comprise 1 or more of the
 CC epitopes given in AAR70360-69 or their variants or mimetics. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
 |||
 Db 9 KKP 11

RESULT 25

AAR52710

ID AAR52710 standard; protein; 11 AA.

XX

AC AAR52710;

XX

DT 25-MAR-2003 (revised)

DT 06-JAN-1995 (first entry)

XX

DE Enkephalinase peptide fragment KC31.

XX

KW Human; enkephalinase; neutral endopeptidase; kidney; intestine; kinin;

KW kidney brush border neutral proteinase; pituitary; brain; lymph nodes;

KW neutrophils; enkephalins; tachykinins.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "Unidentified amino acid"

XX

PN EP596355-A1.

XX

PD 11-MAY-1994.
 XX
 PF 23-DEC-1987; 93EP-00117230.
 XX
 PR 24-DEC-1986; 86US-00946566.
 PR 12-JAN-1987; 87US-00002478.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Malfroy-Camine B, Schofield PR;
 XX
 DR WPI; 1994-152785/19.
 XX
 PT Method for assay of enkephalinase using dansylated peptide(s) - for
 PT identification of recombinant enkephalinase.
 XX
 PS Example 1; Page 13; 6lpp; English.
 XX
 CC The sequences given in AAR52709-14 represents peptide fragments of rat
 CC enkephalinase derived from rat kidney. These peptides were generated by
 CC Lysine-C proteinase digestion of enkephalinase and HPLC purification.
 CC Enkephalinase is a neutral endopeptidase or kidney brush border neutral
 CC proteinase. It has been isolated from the kidney, intestine, pituitary,
 CC brain and lymph nodes, and has been detected in many peripheral organs
 CC and in human neutrophils. The distribution of enkephalinase in the brain
 CC closely parallels that of the enkephalins. Mammalian enkephalinase may be
 CC used in the treatment of various pathological disorders associated with
 CC various endogenous peptides, eg. tachykinins and kinins. (Updated on 25-
 CC MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
 |||
 Db 9 KPK 11

RESULT 26

AAW06227

ID AAW06227 standard; peptide; 11 AA.

XX

AC AAW06227;

XX

DT 20-JAN-1997 (first entry)

XX

DE LHRH antagonist peptide #9.

XX

KW Leuteinising hormone-releasing hormone; LHRH; antagonist; hirsutism;

KW acyl functional group; gonadotrophin; androgen; contraception;

KW benign prostatic hyperplasia; breast cancer; prostate cancer;

KW ovarian cancer; cryptorchidism; gastric motility disorder; dysmenorrhoea;

KW endometriosis; puberty.

XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-(R,S)-tetrahydrofuran-2-oyl-Gly"
FT Modified-site 2
FT /label= OTHER
FT /note= "D-3-(naphth-2-yl)Ala"
FT Modified-site 3
FT /note= "D-3-(4-chlorophenyl)Ala"
FT Modified-site 4
FT /label= OTHER
FT /note= "D-3-(pyrid-3-yl)Ala"
FT Modified-site 6
FT /note= "Lys(3-amino-1,2,4-triazol-5-yl)"
FT Modified-site 7
FT /note= "Lys(3-amino-1,2,4-triazol-5-yl), D-form residue"
FT Modified-site 9
FT /note= "Lys(N-epsilon-isopropyl)"
FT Modified-site 11
FT /label= MeGly
FT /note= "Amidated C-terminal"
XX
PN WO9504541-A1.
XX
PD 16-FEB-1995.
XX
PF 29-JUL-1994; 94WO-US008678.
XX
PR 06-AUG-1993; 93US-00103022.
PR 27-JUL-1994; 94US-00279677.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Haviv F, Fitzpatrick TD, Swenson RE, Nichols CJ, Mort NA;
XX
DR WPI; 1995-090680/12.
XX
PT New N-terminal acylated deca- and undeca:peptide cpds. - useful as potent
PT antagonists of LHRH, e.g. for treating benign prostatic hyperplasia,
PT tumours, hirsutism, gastric motility disorders, etc.
XX
PS Claim 4; Page 86-87; 92pp; English.
XX
CC The sequences given in AAW06219-31 represent synthetic peptides which act
CC as leuteinising hormone-releasing hormone (LHRH) antagonists. These
CC peptides represent analogues of LHRH which have been modified at the N-
CC terminus by addition of either an acyl functional group or an acyl
CC functional group together with an additional aminoacyl residue. The LHRH
CC antagonists are useful for suppressing levels of gonadotrophins and
CC androgens in mammals. They may be used e.g. in treatment of benign
CC prostatic hyperplasia, breast, prostate or ovary tumours, cryptorchidism,
CC hirsutism, gastric motility disorders, dysmenorrhoea or endometriosis, to
CC delay puberty, or in contraception
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
 |||
 Db 5 SKK 7

RESULT 27

AAW06228

ID AAW06228 standard; peptide; 11 AA.

XX

AC AAW06228;

XX

DT 20-JAN-1997 (first entry)

XX

DE LHRH antagonist peptide #10.

XX

KW Leuteinising hormone-releasing hormone; LHRH; antagonist; hirsutism;

KW acyl functional group; gonadotrophin; androgen; contraception;

KW benign prostatic hyperplasia; breast cancer; prostate cancer;

KW ovarian cancer; cryptorchidism; gastric motility disorder; dysmenorrhoea;

KW endometriosis; puberty.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-(R,S)-tetrahydrofur-2-oyl-Gly"

FT Modified-site 2

FT /label= OTHER

FT /note= "D-3-(naphth-2-yl)Ala"

FT Modified-site 3

FT /note= "D-3-(4-chlorophenyl)Ala"

FT Modified-site 4

FT /label= OTHER

FT /note= "D-3-(pyrid-3-yl)Ala"

FT Modified-site 6

FT /note= "Lys(3-amino-1,2,4-triazol-5-yl) or Lys(nic)"

FT Modified-site 7

FT /note= "Lys(3-amino-1,2,4-triazol-5-yl) or Lys(nic), D-form residue"

FT Modified-site 9

FT /note= "Lys(N-epsilon-isopropyl)"

FT Modified-site 11

FT /note= "DAla-NH2"

XX

PN WO9504541-A1.

XX

PD 16-FEB-1995.

XX

PF 29-JUL-1994; 94WO-US008678.

XX

PR 06-AUG-1993; 93US-00103022.

PR 27-JUL-1994; 94US-00279677.

XX
PA (ABBO) ABBOTT LAB.
XX
PI Haviv F, Fitzpatrick TD, Swenson RE, Nichols CJ, Mort NA;
XX
DR WPI; 1995-090680/12.
XX
PT New N-terminal acylated deca- and undeca:peptide cpds. - useful as potent
PT antagonists of LHRH, e.g. for treating benign prostatic hyperplasia,
PT tumours, hirsutism, gastric motility disorders, etc.
XX
PS Claim 4; Page 86-87; 92pp; English.
XX
CC The sequences given in AAW06219-31 represent synthetic peptides which act
CC as leuteinising hormone-releasing hormone (LHRH) antagonists. These
CC peptides represent analogues of LHRH which have been modified at the N-
CC terminus by addition of either an acyl functional group or an acyl
CC functional group together with an additional aminoacyl residue. The LHRH
CC antagonists are useful for suppressing levels of gonadotrophins and
CC androgens in mammals. They may be used e.g. in treatment of benign
CC prostatic hyperplasia, breast, prostate or ovary tumours, cryptorchidism,
CC hirsutism, gastric motility disorders, dysmenorrhoea or endometriosis, to
CC delay puberty, or in contraception
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 5 SKK 7

RESULT 28

AAR68911

ID AAR68911 standard; peptide; 11 AA.

XX

AC AAR68911;

XX

DT 25-MAR-2003 (revised)

DT 06-AUG-1995 (first entry)

XX

DE Factor-VII-derived peptide fragment FVII-1.

XX

KW Factor-VII; blood-clotting factor; thrombosis; angina;

KW cerebrovascular disease; pulmonary embolism; heart disease.

XX

OS Synthetic.

XX

PN WO9500541-A1.

XX

PD 05-JAN-1995.

XX

PF 17-JUN-1994; 94WO-GB001315.

XX

PR 18-JUN-1993; 93GB-00012601.
 PR 10-MAY-1994; 94GB-00009335.
 XX
 PA (HAFS-) HAFSLUND NYCOMED AS.
 PA (HOLM/) HOLMES M J.
 XX
 PI Stephens RW, Orning L, Sakariassen KS;
 XX
 DR WPI; 1995-052003/07.
 XX
 PT Factor VII-derived peptide compounds - useful for preventing/inhibiting
 PT binding of tissue factor to factor VII.
 XX
 PS Disclosure; Page 20; 6lpp; English.
 XX
 CC This peptide fragment is useful for preparing pharmaceutical compositions
 CC for prevention or inhibition of Factor-VII binding to tissue factor. It
 CC is useful for treating or preventing blood clotting disorders in humans
 CC and animals, e.g. thrombosis, angina, cerebrovascular disease or
 CC pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
 |||
 Db 8 KRN 10

RESULT 29

AAR67858

ID AAR67858 standard; peptide; 11 AA.

XX

AC AAR67858;

XX

DT 25-MAR-2003 (revised)

DT 07-SEP-1995 (first entry)

XX

DE FVII/TF multi-protein complex inhibition test peptide FVII-1.

XX

KW Factor VII; Factor 7; blood clotting factor; multi-protein complex;
 KW human tissue factor; FVII/TF; assay.

XX

OS Synthetic.

XX

PN W09500847-A1.

XX

PD 05-JAN-1995.

XX

PF 17-JUN-1994; 94WO-GB001314.

XX

PR 18-JUN-1993; 93GB-00012638.

XX

PA (HAFS-) HAFSLUND NYCOMED AS.

PA (HOLM/) HOLMES M J.
 XX
 PI Stephens R, Oerning L, Sakariassen K;
 XX
 DR WPI; 1995-052226/07.
 XX
 PT Immunoassay for multi-protein complexes - used to detect malfunction in
 PT formation of complexes in an individual, e.g. due to genetic or
 PT physiological disorders.
 XX
 PS Example 2; Page 8; 19pp; English.
 XX
 CC Synthetic peptides (AAR67858-R67865) were individually assayed as test
 CC substances to ascertain their effect on the formation of the blood-
 CC clotting factor VII/tissue factor multi-protein complex. Of the peptides
 CC tested, the most inhibition was obtained with cyclic peptides
 CC representing the ring structures present in the FVII growth factor
 CC domains (i.e. AAR67861, AAR67864 and AAR67863). Peptide AAR67858, a
 CC linear peptide corresp. to residues 136-146 from a region close to the
 CC site of cleavage which activates FVII also had good inhibitory activity.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRN 8
 |||
 Db 8 KRN 10

RESULT 30
 AAW21329

ID AAW21329 standard; peptide; 11 AA.
 XX
 AC AAW21329;
 XX
 DT 29-JUL-1997 (first entry)
 XX
 DE Glucagon precursor derived signal oligopeptide #34.
 XX
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
 KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
 KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
 KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
 XX
 OS Homo sapiens.
 XX

PN WO9519568-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 12-JAN-1995; 95WO-US000575.
 XX
 PR 14-JAN-1994; 94US-00182248.
 XX
 PA (RATH/) RATH M.
 XX
 PI Rath M;
 XX
 DR WPI; 1995-263953/34.
 XX
 PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
 PT regions of max. hydrophilicity, used in modulating communication between
 PT protein(s).
 XX
 PS Claim 5; Page 44; 88pp; English.
 XX
 CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
 CC peptides. These signal oligopeptides are localised on the surface of the
 CC protein and are represented by the hydrophilicity maxima of the protein.
 CC These peptides are enriched in charged amino acids arranged with neutral
 CC spacer amino acids. The specific signal character of these oligopeptides
 CC is determined by a characteristic combination of conformation and charge
 CC within the signal sequence. These oligopeptides may be used as vaccines
 CC in the treatment of human disease, as competitive inhibitors to prevent
 CC or reduce the metabolic action or interaction of a selected protein by
 CC blocking its specific signal sequences, or as therapeutic agents to
 CC function as feedback regulators to reduce synthesis rate of a selected
 CC protein. These peptides may be modified by omitting one or more amino
 CC acids at the N- and/or C-terminal, by substituting one or more amino
 CC acids without consideration of charge and polarity, by substituting one
 CC or more amino acids with amino acid residues with similar charge and/or
 CC polarity, by omitting one or more amino acids or a combination of these
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRN 8
 |||
 Db 2 KRN 4

RESULT 31
 AAW21466
 ID AAW21466 standard; peptide; 11 AA.
 XX
 AC AAW21466;
 XX
 DT 29-JUL-1997 (first entry)
 XX
 DE Islet amyloid precursor derived signal oligopeptide #4.

XX
KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX
OS Homo sapiens.

XX
PN WO9519568-A1.

XX
PD 20-JUL-1995.

XX
PF 12-JAN-1995; 95WO-US000575.

XX
PR 14-JAN-1994; 94US-00182248.

XX
PA (RATH/) RATH M.

XX
PI Rath M;

XX
DR WPI; 1995-263953/34.

XX
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).

XX
PS Claim 5; Page 67; 88pp; English.

XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
|||
Db 1 KRN 3

RESULT 32

AAW21467

ID AAW21467 standard; peptide; 11 AA.

XX

AC AAW21467;

XX

DT 29-JUL-1997 (first entry)

XX

DE Islet amyloid precursor derived signal oligopeptide #5.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberein precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Homo sapiens.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).

XX

PS Claim 5; Page 67; 88pp; English.

XX

CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines

CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
|||
Db 1 KRN 3

RESULT 33

AAR84537

ID AAR84537 standard; peptide; 11 AA.

XX

AC AAR84537;

XX

DT 06-JUN-1996 (first entry)

XX

DE Hepatitis C virus core antigen (amino acids 8-18).

XX

KW Tailor-made; antigen/antibody specificity exchanger; HIV infection;

KW heavy chain; complementarity determining region; CDR;

KW human immunodeficiency virus; variable loop 3 domain; redirecting;

KW epitope; HCV; hepatitis C virus; core protein.

XX

OS Synthetic.

XX

PN WO9529938-A1.

XX

PD 09-NOV-1995.

XX

PF 27-APR-1995; 95WO-SE000468.

XX

PR 28-APR-1994; 94SE-00001460.

XX

PA (FERR) FERRING AB.

XX

PI Saellberg M;

XX

DR WPI; 1995-393040/50.

XX

PT Antigen-antibody specificity exchanger - used in a method to redirect a
PT patients antibodies against polio:virus to fight HIV infection in the
PT patient.

XX

PS Claim 7; Page 35; 38pp; English.

XX
 CC An antigen/antibody specificity exchanger comprises an antibody- derived
 CC amino acid sequence (A) which specifically binds to a particular antigen,
 CC linked to an amino acid sequence (C) to which a particular antibody
 CC binds. The present sequence is a preferred example of a type (C) sequence
 CC ; it is an epitope from hepatitis C virus. Preferred type (A) sequences
 CC are complementarity determining regions from e.g. anti-HIV-1 antibodies.
 CC The specificity exchanger can redirect antibodies already present in a
 CC patient and raised against a particular antigen, to fight a different
 CC antigen. For example, it was shown that anti-poliovirus antibodies could
 CC be redirected to fight HIV
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
 |||
 Db 5 KRN 7

RESULT 34

AAR67274

ID AAR67274 standard; peptide; 11 AA.

XX

AC AAR67274;

XX

DT 25-MAR-2003 (revised)

DT 01-AUG-1995 (first entry)

XX

DE Synthetic human/bovine FGF acidic peptide, 1-11.

XX

KW Cell growth factor; viscoelastic solution; fibroblastic growth factor;

KW FGF; epidermal growth factor; EGF; buffered solution; lubrication;

KW carboxypropyl methylcellulose; cellulose gum; dextran; dextran sulphate;

KW chondroitin sulphate; sodium hyaluronate; osmolarity; mitogenic;

KW wound healing; cell protection; cell coating; surgery; tissue space;

KW hydroxypropyl methylcellulose; manipulation.

XX

OS Synthetic.

XX

PN US5366964-A.

XX

PD 22-NOV-1994.

XX

PF 13-NOV-1989; 89US-00434305.

XX

PR 15-DEC-1988; 88US-00284533.

XX

PA (LIND/) LINDSTROM R L.

PA (SKEL/) SKELNIK D.

XX

PI Skelnik D, Lindstrom RL;

XX

DR WPI; 1995-005865/01.

XX
PT Viscoelastic soln. contg. hydroxypropyl methylcellulose, sodium
PT hyaluronate, chondroitin sulphate and growth factors - used as a surgical
PT soln. to promote wound healing, e.g. of corneal cells.
XX
PS Disclosure; Col 4; 8pp; English.
XX
CC The sequences given in AAR67273-76 are cell growth factors which may be
CC used in the viscoelastic solution of the invention. The peptides are
CC derived from fibroblastic growth factor (FGF) and epidermal growth factor
CC (EGF). The viscoelastic solution also comprises a buffered solution which
CC is pref. a buffered balanced salt solution, at least 1 of hydroxy- or
CC carboxypropyl methylcellulose, a cellulose gum, dextran or dextran
CC sulphate, chondroitin sulphate, and sodium hyaluronate. It has a pH of 6-
CC 8 and an osmolarity of 200-400 mOsmol/l. The growth factors are mitogenic
CC in vitro for a wide range of tissues and the viscoelastic soln. may be
CC used as a surgical soln. which is in direct contact with cells undergoing
CC wound healing. It also provides a cell protection and cell coating during
CC surgery. The soln. provides maintenance of tissue space, hydroxypropyl
CC methylcellulose and chondroitin sulphate lubricate the tissue, while
CC sodium hyaluronate provides tissue manipulation. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
| | |
Db 9 KKP 11

RESULT 35

AAR99265

ID AAR99265 standard; peptide; 11 AA.

XX

AC AAR99265;

XX

DT 07-NOV-1996 (first entry)

XX

DE Myosin light chain-1 amino acids 34-44 used for MAb 39-15 prodn.

XX

KW Myosin light chain; ventricular; heart; cardiac; angina; infarction; MAb;
KW monoclonal antibody; aa; amino acid; branched; polylysine core;
KW octameric; antigenic; hybridoma.

XX

OS Synthetic.

XX

PN WO9610078-A1.

XX

PD 04-APR-1996.

XX

PF 28-SEP-1995; 95WO-IB000808.

XX

PR 28-SEP-1994; 94US-00314202.

XX
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
XX
PI Takahashi M, Jackowski G;
XX
DR WPI; 1996-200917/20.
XX
PT Anti-cardiac myosin light chain monoclonal antibody - useful to detect
PT cardiac myosin in patients with cardiac muscle damage.
XX
PS Example 1; Page 14; 31pp; English.
XX
CC AAR99265 corresponds to residues 34-44 of human ventricular myosin light
CC chain 1 (MLC-1). This peptide was used for the production of a high
CC affinity monoclonal antibody, Mab 39-15, against MLC-1. Residues 34-44 of
CC MLC-1 are highly conserved and this sequence may be used alone to produce
CC Mab 39-15 or as an octameric branched peptide contg. eight copies of the
CC peptide linked C-terminally to a polylysine core. Mab 39-15 is useful to
CC detect myosin light chains (esp. cardiac MLC), in a blood, serum or
CC plasma sample of patients with cardiac muscle damage e.g. myocardial
CC infarction or unstable angina patients
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 6 ASK 8

RESULT 36
AAW05350
ID AAW05350 standard; peptide; 11 AA.
XX
AC AAW05350;
XX
DT 30-APR-1997 (first entry)
XX
DE Residues 363-373 of p53.
XX
KW Human; p53; cell proliferation; cell death; regulator; tumour; psoriasis;
KW negative regulatory region; DNA damaging agent; transplant rejection;
KW abnormal cell proliferation; atherosclerosis; cancer; autoimmune disease;
KW arterial restenosis; immune response; apoptosis; inducer; therapy;
KW proliferating lymphocytes.
XX
OS Homo sapiens.
XX
PN WO9625434-A1.
XX
PD 22-AUG-1996.
XX
PF 16-FEB-1996; 96WO-US001535.
XX

PR 16-FEB-1995; 95US-00392542.

XX

PA (WIST-) WISTAR INST.

PA (FARB) BAYER CORP.

XX

PI Halazonetis T, Hartwig W;

XX

DR WPI; 1996-393345/39.

XX

PT New human p53-isomorphic peptide(s) and peptido:mimetic cpds. - used for
PT activating p53 function, e.g. for treating tumours, cancers, psoriasis,
PT etc.

XX

PS Claim 2; Page 35; 55pp; English.

XX

CC AAW05350-W05364 represent the p53 (see AAW05344 for full length wild type
CC sequence) peptides of the invention. The p53 protein functions to
CC regulate cell proliferation and cell death, and is mutated in more than
CC half of all human tumours. These sequences are used to activate the DNA
CC binding activity of wild type p53, and p53 mutants (see AAW05345-W05349).
CC The peptides of the invention consist of at least four sequential amino
CC acids from a negative regulatory region which maps to residues 361-383 of
CC p53. These sequences preferably contain four amino acids from a non-human
CC p53 sequence, contain D-form amino acids, and can also be cyclic
CC peptides. The sequences retain the structural characteristics of the
CC original peptides, but the modifications render them less susceptible to
CC cleavage by proteases and exopeptidases. As these sequences activate p53
CC DNA binding, they can be used to identify p53 mutants. The peptides can
CC also be used for treating a patient with a tumour expressing a p53 mutant
CC whose ability to bind DNA may be activated by one of the peptides. They
CC can also be used for treating conditions such as exposure to DNA damaging
CC agents, abnormal cell proliferation characteristic of psoriasis,
CC atherosclerosis, cancer, arterial restenosis, autoimmune diseases and
CC undesirable immune responses accompanying rejection of a transplant. The
CC peptides can also induce apoptosis of specific cells, such as
CC proliferating lymphocytes

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4

|||

Db 9 SKK 11

RESULT 37

AAR92022

ID AAR92022 standard; peptide; 11 AA.

XX

AC AAR92022;

XX

DT 18-SEP-1996 (first entry)

XX

DE Multiple antigenic peptide based on cluster-w4 polypeptide.

XX
 KW Antigen; cluster-w4 polypeptide; human small cell lung carcinoma;
 KW cell line H69; antibody.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 10
 FT /note= "Is attached via a peptide linkage to the C
 FT terminal of the peptide sequence: KVAGGALQS"
 FT Modified-site 11
 FT /note= "Is attached via a peptide linkage to the C
 FT terminal of the peptide sequence: KVAGGALQS (KVAGGALQS) K"
 XX
 PN WO9604312-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 31-JUL-1995; 95WO-GB001795.
 XX
 PR 01-AUG-1994; 94GB-00015492.
 XX
 PA (CLLT) CELLTECH THERAPEUTICS LTD.
 XX
 PI Lawson AD;
 XX
 DR WPI; 1996-129341/13.
 XX
 PT Binding agent for cluster-w4 polypeptide of small cell lung carcinoma -
 PT pref. antibody, has low affinity for native CD24, useful in diagnosis and
 PT treatment.
 XX
 PS Example 1; Page 12; 25pp; English.
 XX
 CC The sequences given in AAR92022-23 represent antigenic peptides based on
 CC the cluster-w4 polypeptide from human small cell lung carcinoma cell line
 CC H69 which is known to carry the Val57 mutation. These peptides are
 CC examples of the generic sequence given in AAR98500. These peptides were
 CC used in the isolation of an agent, pref. an antibody, which is used in
 CC the treatment and diagnosis of small cell lung carcinoma
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
 |||
 Db 9 SKK 11

RESULT 38

AAW41825

ID AAW41825 standard; peptide; 11 AA.

XX

AC AAW41825;

XX
 DT 14-MAY-1998 (first entry)
 XX
 DE Modified B. burgdorferi sensu lato OspC C-terminal peptide.
 XX
 KW Sensus lato; outer surface protein C; OspC; diagnosis; Lyme disease;
 KW vaccine; infection.
 XX
 OS Borrelia burgdorferi.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "6-aminohexanoic acid"
 XX
 PN WO9742221-A1.
 XX
 PD 13-NOV-1997.
 XX
 PF 02-MAY-1997; 97WO-DK000203.
 XX
 PR 02-MAY-1996; 96DK-00000526.
 XX
 PA (STAT-) STATENS SERUMINSTITUT.
 XX
 PI Mathiesen MJ, Theisen M, Holm A, Ostergaard S;
 XX
 DR WPI; 1997-558908/51.
 XX
 PT Detecting previous sensitisation to the OspC protein of Borellia
 PT burgdorferi - by detecting immunoreactivity between patient T cells or
 PT immunoglobulins and C-terminal peptide of the protein.
 XX
 PS Example; Page 40; 95pp; English.
 XX
 CC The present sequence was used in the development of a novel method for
 CC the identification of a patient's previous sensitisation to Borellia
 CC burgdorferi sensu lato outer surface protein C (OspC). The method
 CC comprises reacting immunoglobulin (Ig) or T cells from the patient with a
 CC polypeptide of at most 60 amino acids containing a peptide with at least
 CC 50% identity to the B. burgdorferi derived sequence AAW41821, or its
 CC subsequences of at least 5 amino acids. The degree of immunological
 CC reactivity between the polypeptide and Ig or T cells is measured and
 CC significant reactivity is indicative of sensitisation. The method can be
 CC used to diagnose Lyme disease and is based on reactivity with antibodies
 CC against the OspC protein. The test can be done in vitro or in vivo, e.g.
 CC as a skin test. Vaccine compositions comprising the polypeptide can be
 CC used to protect humans and other animals against B. burgdorferi
 CC infection. The polypeptide provides higher sensitivity than full-length
 CC OspC, and so is better at detecting infection in its early stages,
 CC especially when combined with the known assay for flagellar proteins. The
 CC seven carboxy-terminal residues of AAW41821 represent an epitope
 CC essential for human immune response to OspC. The polypeptide is also
 CC easier to prepare and purify than (nearly) full-length protein,
 CC facilitating standardisation of the assay, and is less cross-reactive
 CC with antibodies raised against other antigens. The small size of the
 CC polypeptide allows a high density of binding sites to be created on a

CC solid support. Incorporation of non-natural amino acid into the
CC polypeptide increases its resistance to peptidases when used in vivo
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 9 KKP 11

RESULT 39

AAW10458

ID AAW10458 standard; peptide; 11 AA.

XX

AC AAW10458;

XX

DT 25-MAR-2003 (revised)

DT 11-AUG-1997 (first entry)

XX

DE Human growth hormone Gln-22 substitution peptide.

XX

KW Active site; active domain; growth hormone; somatogenic receptor;
KW mutagenesis.

XX

OS Synthetic.

XX

PN US5580723-A.

XX

PD 03-DEC-1996.

XX

PF 02-FEB-1994; 94US-00190723.

XX

PR 28-OCT-1988; 88US-00264611.

PR 26-OCT-1989; 89US-00428066.

PR 27-APR-1992; 92US-00875204.

PR 13-OCT-1992; 92US-00960227.

XX

PA (GETH) GENENTECH INC.

XX

PI Cunningham BC, Wells JA;

XX

DR WPI; 1997-033563/03.

XX

PT Identification of unknown active domains in polypeptide(s) - useful for
PT analysis of structure and function of hormones, etc.

XX

PS Disclosure; Col 26; 86pp; English.

XX

CC Substitution peptides (AAW10441-62) were used to identify specific amino
CC acid residues in human growth hormone (hGH) (AAW10425) which are expected
CC to product hGH variants having altered biological functions. The method
CC involved substituting selected amino acid segments of hGH with analogous
CC segments from analogue polypeptides (human placenta lactogen, human

CC prolactin and pig growth hormone) and examining the effect of the
 CC substns. on interaction with the soluble hGH receptor (see also
 CC AAW10426). Once active site domains had been detd., amino acid residues
 CC within these domains were replaced sequentially with alanine, and the
 CC effects on interaction with the hGH receptor were again examined. Gln-22
 CC was identified by this method; the preferred amino acid substn. for this
 CC residue is given in AAW10458. Active site residues have also been
 CC identified (see also AAW10427-40). (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
 |||
 Db 7 SKK 9

RESULT 40

AAW10460

ID AAW10460 standard; peptide; 11 AA.

XX

AC AAW10460;

XX

DT 25-MAR-2003 (revised)

DT 11-AUG-1997 (first entry)

XX

DE Human growth hormone Gln-29 substitution peptide.

XX

KW Active site; active domain; growth hormone; somatogenic receptor;

KW mutagenesis.

XX

OS Synthetic.

XX

PN US5580723-A.

XX

PD 03-DEC-1996.

XX

PF 02-FEB-1994; 94US-00190723.

XX

PR 28-OCT-1988; 88US-00264611.

PR 26-OCT-1989; 89US-00428066.

PR 27-APR-1992; 92US-00875204.

PR 13-OCT-1992; 92US-00960227.

XX

PA (GETH) GENENTECH INC.

XX

PI Cunningham BC, Wells JA;

XX

DR WPI; 1997-033563/03.

XX

PT Identification of unknown active domains in polypeptide(s) - useful for
 PT analysis of structure and function of hormones, etc.

XX

PS Disclosure; Col 26; 86pp; English.

XX

CC Substitution peptides (AAW10441-62) were used to identify specific amino
CC acid residues in human growth hormone (hGH) (AAW10425) which are expected
CC to product hGH variants having altered biological functions. The method
CC involved substituting selected amino acid segments of hGH with analogous
CC segments from analogue polypeptides (human placenta lactogen, human
CC prolactin and pig growth hormone) and examining the effect of the
CC substns. on interaction with the soluble hGH receptor (see also
CC AAW10426). Once active site domains had been detd., amino acid residues
CC within these domains were replaced sequentially with alanine, and the
CC effects on interaction with the hGH receptor were again examined. Gln-29
CC was identified by this method; the preferred amino acid substn. for this
CC residue is given in AAW10460. Active site residues have also been
CC identified (see also AAW10427-40). (Updated on 25-MAR-2003 to correct PF
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 7 SKK 9

RESULT 41

AAW33181

ID AAW33181 standard; peptide; 11 AA.

XX

AC AAW33181;

XX

DT 29-JAN-1998 (first entry)

XX

DE Mono-DTPA-Lys1 Substance P.

XX

KW Substance P; radiolabel; diagnostic imaging; therapy; mono-DTPA-Lys1.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "DTPA-Lys"

FT Modified-site 11

FT /note= "amidated"

XX

PN WO9640292-A1.

XX

PD 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US009706.

XX

PR 07-JUN-1995; 95US-00480372.

XX

PA (MLCW) MALLINCKRODT MEDICAL INC.

XX
 PI Srinivasan A;
 XX
 DR WPI; 1997-087027/08.
 XX
 PT Prepn. of pure radio:labelled peptide, e.g. for diagnostic imaging - by
 PT combining protected poly:amino:carboxylate ligand with peptide and
 PT forming complex with radionuclide.
 XX
 PS Example 4; Page 12; 20pp; English.
 XX
 CC Preparing a radiolabelled peptide composition, comprises combining a
 CC triamine or diamine chelating agent with a peptide, e.g. the present
 CC peptide, in a solid phase peptide synthesiser, and complexing a
 CC radionuclide with the chelate-peptide conjugate. Radiolabelled peptides
 CC or peptidomimetics can be used as diagnostic imaging agents, or in
 CC therapeutic applications, e.g. iodine(111) labelled pentatreotide can be
 CC used for somatostatin receptor imaging of neuroendocrine tumours. The
 CC radiolabelled products are obtained efficiently and inexpensively in high
 CC purity. The protected polyaminocarboxylate ligands can be added to the
 CC peptide by standard solution or solid phase peptide synthesis and
 CC deprotected with conventional reagents to give only the mono-addition
 CC product, free of di-addition product impurities. The deprotected product
 CC can be labelled with medically useful radionuclides, e.g lanthanides or
 CC actinides, at any desired location. Pre-derivatisation of individual
 CC amino acids is not required
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
 |||
 Db 1 KPK 3

RESULT 42

AAW23266

ID AAW23266 standard; peptide; 11 AA.

XX

AC AAW23266;

XX

DT 03-NOV-1997 (first entry)

XX

DE Tumour necrosis factor alpha inhibiting peptide.

XX

KW Tumour necrosis factor; alpha; TNF-alpha; inhibition; treatment;
 KW mediation; disorder; septic shock; bacterium; virus; fungus; infection;
 KW autoimmune; disease; alcohol induced hepatitis; sarcoiditis; Crohn's;
 KW disseminated intravascular coagulation; graft versus host; Rawasaki's;
 KW tumour; bacteria.

XX

OS Synthetic.

XX

PN US5641751-A.

XX
 PD 24-JUN-1997.
 XX
 PF 01-MAY-1995; 95US-00432694.
 XX
 PR 01-MAY-1995; 95US-00432694.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Heavner GA;
 XX
 DR WPI; 1997-340972/31.
 XX
 PT Peptide inhibiting tumour necrosis factor alpha - useful for treating
 PT septic shock, infections, autoimmune diseases, etc.
 XX
 PS Disclosure; Col 23-24; 15pp; English.
 XX
 CC The present peptide is a tumour necrosis factor alpha (TNF-alpha)
 CC inhibitor, which can be used to treat TNF-alpha mediated disorders, e.g.
 CC septic shock, bacterial, viral and fungal infections, autoimmune
 CC diseases, alcohol induced hepatitis, sarcoiditis, Crohn's disease,
 CC disseminated intravascular coagulation, graft versus host disease,
 CC Rawasaki's disease and TNF-alpha secreting tumours. The peptide is
 CC preferably given as a daily dose of 1-1000, preferably 1-10 mg/kg
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
 |||
 Db 2 ASK 4

RESULT 43

AAW39588

ID AAW39588 standard; peptide; 11 AA.

XX

AC AAW39588;

XX

DT 11-JUN-1998 (first entry)

XX

DE Human melanoma associated protein tyrosinase peptide (pos. 116-126).

XX

KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
 KW vaccine; immunogenic; major histocompatiblilty complex; MHC; B cell;
 KW disease; anti-tumour; anti-viral.

XX

OS Homo sapiens.

XX

PN WO9741440-A1.

XX

PD 06-NOV-1997.

XX

PF 28-APR-1997; 97WO-NL000229.

XX

PR 26-APR-1996; 96EP-00201145.

PR 23-DEC-1996; 96EP-00203670.

XX

PA (UYLE-) RIJKSUNIV LEIDEN.

PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.

XX

PI Van Der Burg SH, Kast WM, Toes REM, Offringa R, Melief CJM;

XX

DR WPI; 1997-549891/50.

XX

PT Method of selecting T cell peptide epitope(s) - by measuring the

PT stability of HLA class I-peptide complexes on intact B cells.

XX

PS Example 3; Page 75; 109pp; English.

XX

CC Peptides AAW39430-W39734 are used in a novel method for the selection of
CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
CC method involves the identification of peptide sequences capable of
CC binding to an HLA (human leukocyte antigen) class I molecule and
CC measuring the binding of this epitope peptide to the HLA class I peptide.
CC The stability of binding of the peptide and MHC (major histocompatibility
CC complex) class I molecule is measured on intact human B cells carrying
CC the MHC molecule at their cell surfaces. The method can be used to select
CC peptide epitopes for generating vaccines against a disease associated
CC with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are
CC especially T-cell peptide epitopes with strong anti-tumour and anti-viral
CC immune responses. Peptide AAW39588 is derived from the human melanoma
CC associated protein tyrosinase which is capable of upregulating HLA-A*0201
CC molecules on T2 cells

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RNI 9

|||

Db 6 RNI 8

RESULT 44

AAW09910

ID AAW09910 standard; peptide; 11 AA.

XX

AC AAW09910;

XX

DT 16-OCT-1997 (first entry)

XX

DE Prostate specific membrane antigen peptide PSM-P27.

XX

KW Prostate specific membrane antigen; PSMA; prostate specific antigen; PSA;

KW prostate cancer; adoptive cellular immunotherapy; therapy; vaccine.

XX

OS Homo sapiens.

XX
 PN WO9704802-A1.
 XX
 PD 13-FEB-1997.
 XX
 PF 29-JUL-1996; 96WO-US012389.
 XX
 PR 31-JUL-1995; 95US-00509254.
 XX
 PA (PACI-) PACIFIC NORTHWEST CANCER FOUND.
 XX
 PI Murphy GP, Boynton AL, Tjoa BA;
 XX
 DR WPI; 1997-145375/13.
 XX
 PT Use of dendritic cells for prostate cancer immuno:therapy - the cells are
 PT exposed to prostate cancer antigen, then administered to the patient
 PT where they activate and proliferate T-cells.
 XX
 PS Claim 3; Page 47; 69pp; English.
 XX
 CC Peptide PSM-P27 (AAW09910) corresponds to amino acid residues 63-73 of
 CC prostate specific membrane antigen (PSMA). A method for producing a
 CC cancer growth inhibiting response comprises exposing human dendritic
 CC cells (DCs) to PSM-P27 or other PSMA or prostate specific antigen
 CC peptides (see also AAW09889-909 and AAW09911-26), and then administering
 CC the DCs to a prostate cancer patient to activate T cell responses in
 CC vivo. Alternatively, the T cell response is activated in vitro and the T
 CC cells are then administered to the patient. In either case, the DCs are
 CC used to elicit an immunotherapeutic growth inhibiting response against a
 CC primary or metastatic prostate tumour. PSM-P27 was selected to be
 CC presented by DCs to activate T cells of a patient which match the A11
 CC haplotype
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
 |||
 Db 7 NIK 9

RESULT 45

AAY22688

ID AAY22688 standard; peptide; 11 AA.

XX

AC AAY22688;

XX

DT 13-AUG-1999 (first entry)

XX

DE Neurokinin receptor antagonist.

XX

KW Bradykinin antagonist; lung cancer cell growth; apoptosis; cancer;

KW allergic reaction; arthritis; asthma; sepsis; viral rhinitis;

KW inflammatory bowel disease.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "D-form residue"
 FT Misc-difference 2
 FT /note= "D-form residue"
 FT Misc-difference 7
 FT /note= "D-form residue"
 FT Misc-difference 9
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /label= Nle
 FT /note= "norleucine"
 XX
 PN WO9709347-A1.
 XX
 PD 13-MAR-1997.
 XX
 PF 03-SEP-1996; 96WO-US014113.
 XX
 PR 08-SEP-1995; 95US-00526065.
 XX
 PA (CORT-) CORTECH INC.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Whalley ET, Stewart JM, Chan DC, Gera L;
 XX
 DR WPI; 1997-192841/17.
 XX
 PT Use of bradykinin antagonists and neurokinin receptor antagonists to
 PT inhibit lung cancer cell growth - also new bradykinin antagonist monomers
 PT and dimers.
 XX
 PS Claim 13; Page 38; 51pp; English.
 XX
 CC AAY22686-94 represent neurokinin receptor antagonist, used to make
 CC compounds of the formula BKA-X-Y, where X is a linker, BKA is a
 CC bradykinin antagonist chosen from AAY22658-72, and Y is a neurokinin
 CC receptor antagonist chosen from AAY22686-94. Dimerisation of bradykinin
 CC antagonist peptides increases the potency and stability of the
 CC antagonists. The antagonists are used in methods for inhibiting lung
 CC cancer cell growth. It has been found that the antagonists induce
 CC apoptosis in the treated lung cancer cells. The bradykinin antagonists
 CC are used for treating cancer, especially small cell lung carcinoma. They
 CC are also useful in the treatment of other bradykinin-related conditions
 CC such as allergic reactions, arthritis, asthma, sepsis, viral rhinitis and
 CC inflammatory bowel disease
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
 | | |
Db 3 KPK 5

RESULT 46

AAW10197

ID AAW10197 standard; peptide; 11 AA.

XX

AC AAW10197;

XX

DT 22-JUL-1997 (first entry)

XX

DE Serum immunoregulatory polypeptide C-terminal peptide 7.

XX

KW SIP; Serum immunoregulatory polypeptide; modulator; immune response;

KW activate; suppressor T cell; suppress; lymphocyte proliferation;

KW cell-mediated; humoral immunity; induce tolerance; treatment;

KW allograft rejection; autoimmune disease; graft versus host disease;

KW allergy; cancer; AIDS.

XX

OS Synthetic.

XX

PN WO9638164-A1.

XX

PD 05-DEC-1996.

XX

PF 30-MAY-1996; 96WO-US007925.

XX

PR 31-MAY-1995; 95US-00455645.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Chang Y, Abraham E;

XX

DR WPI; 1997-034096/03.

XX

PT New immuno-regulatory peptide(s) from serum and synthetic analogues -

PT activate suppressor T cells and inhibit prodn. of lymphokine(s) and

PT interleukin-2, for treatment of e.g. allograft rejection, auto-immune

PT disease.

XX

PS Disclosure; Page 8; 35pp; English.

XX

CC Serum immunoregulatory polypeptides (SIP) of the general formula X-

CC AAW10180-Y (where X and Y are 0-10 and 0-110 amino acids resp.). SIP are

CC modulators of the immune response in mammals. The SIPs activate

CC suppressor T cells (reducing lymphocyte proliferation) and suppress

CC prodn. of lymphokines and IL-2 by lymphocytes, i.e. they suppress both

CC cell-mediated and humoral immunity and induce tolerance. They can be used

CC treatment of allograft rejection, autoimmune disease (e.g. systemic lupus

CC erythematosus and rheumatoid arthritis), graft vs. host disease, allergy,

CC cancer (e.g. some forms of leukaemia that require IL-2 at certain stages)

CC and AIDS. SIP can also be used to raise MAb. Apart from diagnostic use

CC (i.e. identifying subjects at risk of developing diseases associated with

CC abnormal immune response or serious infections after traumatic injury),

CC MAb can be used to increase the immune response in immunodeficiency

CC states where SIP is involved. In particular the SIP have a wide
CC therapeutic index without toxic side effects at physiological doses.
CC AAW10191-99 are exemplary Y amino acid sequences

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10

|||

Db 1 NIK 3

RESULT 47

AAW18223

ID AAW18223 standard; peptide; 11 AA.

XX

AC AAW18223;

XX

DT 21-AUG-1997 (first entry)

XX

DE Mycobacterium tuberculosis antigenic peptide A.

XX

KW Vaccine; M.tuberculosis; M.leprae; M.avium; M.bovis.

XX

OS Mycobacterium tuberculosis.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "formyl-Met"

XX

PN WO9640236-A1.

XX

PD 19-DEC-1996.

XX

PF 05-JUN-1996; 96WO-US009473.

XX

PR 07-JUN-1995; 95US-00484169.

XX

PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

XX

PI Potter TA, Dow SW, Orme IM;

XX

DR WPI; 1997-051903/05.

XX

PT Mycobacterium derived antigenic peptide residue, - comprises amino

PT terminal formylated Met, used in Mycobacterium BCG based vaccine.

XX

PS Example 1; Page 55; 93pp; English.

XX

CC The present sequence represents an antigenic peptide, Mycobacterium

CC tuberculosis peptide A, which has an amino terminal formylated Met

CC residue, which is capable of protecting an animal against Mycobacterium

CC infection. A suitable nucleic acid molecule comprises a portion of a

CC Mycobacterium gene, preferably from M.tuberculosis. The peptides and

CC nucleic acids may be used, with an acceptable carrier, in an immunogenic
 CC composition to protect an animal from an intracellular pathogen,
 CC preferably a Mycobacterium species selected from M.tuberculosis,
 CC M.leprae, M.avium and M.bovis. As the compositions of the invention are
 CC not whole cell vaccines, they do not interfere with commonly used
 CC Mycobacterium diagnostic skin tests such as PPD tests. In addition unlike
 CC a whole cell vaccine like BCG, use of a peptide is not accompanied by the
 CC risk of reversion to virulence

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10

|||

Db 5 NIK 7

RESULT 48

AAW10140

ID AAW10140 standard; peptide; 11 AA.

XX

AC AAW10140;

XX

DT 25-MAR-2003 (revised)

DT 02-OCT-1997 (first entry)

XX

DE Hepatitis C virus peptide antigen IIA.

XX

KW Antibody; HCV; immunoassay; vaccine; mimic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "H or a linker arm by which the peptide can be
 FT attached to a carrier or solid phase comprising at least
 FT one amino acid and as many as 60, most frequently 1-20
 FT amino acids, such as Cys, Lys, Tyr, Glu or Asp, or
 FT chemical groups such as biotin or thioglycolic acid; can
 FT be modified by acetylation"

FT Modified-site 11

FT /note= "A bond or a linker arm by which the peptide can
 FT be attached to a carrier or solid phase comprising at
 FT least one amino acid and as many as 60 amino acids, most
 FT frequently 1-10 amino acids, such as Cys, Lys, Tyr, Asp,
 FT or chemical groups such as biotin or thioglycolic acid;
 FT and attached on to that is NH2, OH or a linkage involving
 FT either of these two groups"

XX

PN EP754704-A2.

XX

PD 22-JAN-1997.

XX

PF 14-DEC-1990; 96EP-00201157.

XX
 PR 14-DEC-1990; 90EP-00124241.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Deleys RJ, Pollet D, Maertens G, Van Heuverswyn H;
 XX
 DR WPI; 1997-089256/09.
 XX
 PT Hepatitis C virus peptide mimics - for use in immunoassays, vaccines,
 PT etc.
 XX
 PS Claim 2; Page 38; 65pp; English.
 XX
 CC The present sequence represents a novel synthetic Hepatitis C virus (HCV)
 CC antigen IIA for the detection of antibodies. The peptide contains
 CC modifications at the N- and C-terminal (see features table) with the
 CC condition that if the modification represents an amino acid(s), that they
 CC are different from any naturally occurring HCV flanking regions. The
 CC peptide represents an HCV peptide mimic and may be used as an immunoassay
 CC reagent for detecting antibodies to HCV; for incorporation into vaccines
 CC against HCV; and for raising antibodies against HCV. (Updated on 25-MAR-
 CC 2003 to correct PF field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRN 8
 |||
 Db 5 KRN 7

RESULT 49

AAW35543

ID AAW35543 standard; peptide; 11 AA.

XX

AC AAW35543;

XX

DT 25-MAR-2003 (revised)

DT 22-APR-1998 (first entry)

XX

DE Immunization DNDPC SEQ ID NO:87 from WO9738011.

XX

KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
 KW scaffold; inhibition; metastasis; wound healing; solid phase.

XX

OS Synthetic.

XX

PN WO9738011-A1.

XX

PD 16-OCT-1997.

XX

PF 03-APR-1997; 97WO-DK000146.

XX

PR 03-APR-1996; 96DK-00000398.

XX

PA (PEPR-) PEPRESEARCH AS.

XX

PI Heegaard PMH, Jakobsen PH;

XX

DR WPI; 1997-512645/47.

XX

PT Non-dendritic peptide carrier linked to a solid phase - useful as a
PT diagnostic agent and as a scaffold for production of chemical
PT derivatives.

XX

PS Example 31; Page 156; 262pp; English.

XX

CC A non-dendritic peptide carrier (A) has been developed which is coupled
CC through a linker to a solid phase, forming a complex of (A)-solid phase.
CC Where (A) comprises 10-50 amino acids capable of forming a secondary
CC structure in a benign buffer after liberation from the solid phase, and
CC further the (A)-solid phase complex comprises an immunogenic substance
CC and/or an immune mediator coupled on (A). The present sequence represents
CC a peptide used in an example from the present invention. An (A)-solid
CC phase complex can be used as a scaffold for the production of chemical
CC derivatives, characterised by covalently attaching molecules at
CC attachment points. Alternatively (A) is used as a scaffold-peptide for
CC the incorporation into an Immunostimulating Complex (Iscom) resulting an
CC (A)-Iscom complex which is used for the chemical coupling of antigenic
CC substances in an aqueous solution by conjugation. (A) derivatised with
CC one or more peptides having fibronectin-, laminin- or vitronectin-like
CC binding activities can be used for the promotion of cell-attachment to
CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
CC and for promotion of wound healing. Also a derivatised (A) can be used
CC for the selection of specifically-binding aptamers or as a diagnostic
CC agent. Such diagnostic-(A) molecules could be used to detect molecules
CC derived from or indicative of pregnancy or of a disease, such as an
CC infectious, autoimmune or cancerous disease. (Updated on 25-MAR-2003 to
CC correct PF field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4

|||

Db 7 SKK 9

RESULT 50

AAW12550

ID AAW12550 standard; peptide; 11 AA.

XX

AC AAW12550;

XX

DT 30-APR-1997 (first entry)

XX

DE Japanese cedar pollen allergen-derived peptide 19.

XX
 KW Japanese cedar; sugi; pollen; pollinosis; pollenosis; allergen; allergy;
 KW T-cell epitope; TCR; T-cell receptor; activation; immune tolerance; Cryj.
 XX
 OS Cryptomeria japonica.
 OS Synthetic.
 XX
 PN JP08333391-A.
 XX
 PD 17-DEC-1996.
 XX
 PF 18-JUL-1995; 95JP-00181438.
 XX
 PR 07-APR-1995; 95JP-00082519.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 1997-095487/09.
 XX
 PT Peptide allergen derived from Japanese cedar pollen - causes T cell
 PT response specific to cedar pollen, for treatment of pollenosis.
 XX
 PS Claim 27; Page 20; 21pp; Japanese.
 XX
 CC The present sequence is one of 24 claimed peptides which were synthesised
 CC based on Japanese cedar pollen sequences. This peptide was shown to have
 CC Japanese cedar pollen antigen T cell epitope activity by using T cells
 CC isolated from a cedar pollinosis patient. The peptide produces little or
 CC no anaphylaxis
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
 |||
 Db 2 ASK 4

RESULT 51

AAW39795

ID AAW39795 standard; protein; 11 AA.

XX

AC AAW39795;

XX

DT 11-JUN-1998 (first entry)

XX

DE Tobacco PABFe repeated AT hook.

XX

KW Palindromic element binding factor; PABF; tobacco; cis-acting element;

KW transcription enhancer; heterologous promoter; AATT repeat element;

KW transcription factor; AT hook.

XX

OS Nicotiana tabacum.

XX
 PN WO9749727-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 27-JUN-1997; 97WO-US011156.
 XX
 PR 27-JUN-1996; 96US-00669721.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Lamb CJ, Doerner P, Laible G;
 XX
 DR WPI; 1998-077110/07.
 XX
 PT New isolated enhancer and transcription factor - used for increasing the
 PT recombinant expression of proteins, particularly in plants, e.g. for
 PT increasing production or providing pest resistance.
 XX
 PS Disclosure; Fig 7B; 65pp; English.
 XX
 CC AAW39790-W39796 are AT hook motifs used in the characterisation of a
 CC novel tobacco palindromic element binding factor, (PABF). This PABF binds
 CC to the sequence (AATT)_n where n at least 2. The (AATT)_n sequence has cis-
 CC acting, non-specific enhancer activity. It can be linked to a
 CC heterologous promoter operably linked with a gene to increase expression
 CC of the gene in a cell, particularly in plants. It can provide for
 CC increased expression of proteins such as nutritionally important
 CC proteins, growth promoting factors, proteins for early flowering in
 CC plants, proteins giving protection to the plant under certain
 CC environmental conditions, e.g. proteins conferring resistance to metals
 CC or other toxic substances, such as herbicides or pesticides, stress-
 CC related proteins which confer tolerance to temperature extremes, proteins
 CC conferring resistance to fungi, bacteria, viruses, insects and nematodes,
 CC proteins of specific commercial value, e.g. enzymes involved in metabolic
 CC pathways, such as EPSP synthase. The PABF polypeptides act as
 CC transcription factor and bind to the (AATT) repeat element to further
 CC boost the activity of the enhancer
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
 |||
 Db 3 PKR 5

RESULT 52
 AAW62014
 ID AAW62014 standard; peptide; 11 AA.
 XX
 AC AAW62014;
 XX
 DT 01-OCT-1998 (first entry)

XX
 DE Light chain variable region complementarity determining region 1.
 XX
 KW Complementarity determining region; light chain variable region;
 KW humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;
 KW human CD11a I domain; MHM24 epitope; alpha subunit;
 KW lymphocyte function-associated antigen 1; LFA-1; immunoassay;
 KW in vivo imaging; diagnosis; CD11a-associated disease.
 XX
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO9823761-A1.
 XX
 PD 04-JUN-1998.
 XX
 PF 20-OCT-1997; 97WO-US019041.
 XX
 PR 27-NOV-1996; 96US-00757205.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 1998-322737/28.
 XX
 PT New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
 PT also to treat conditions such as immunological or inflammatory disease.
 XX
 PS Claim 8; Page 2; 66pp; English.
 XX
 CC AAW62014-16 represent complementarity determining regions of the light
 CC chain variable region of humanised antibody MHM24F(ab)-8. The fragments
 CC were used to make a humanised anti-CD11a antibody that binds specifically
 CC to the human CD11a I domain (MHM24 epitope). CD11a refers to the alpha
 CC subunit of lymphocyte function-associated antigen 1 (LFA-1) from any
 CC mammal. The humanised anti-CD11a antibodies are used to determine
 CC presence of CD11a in usual immunoassays or by in vivo imaging,
 CC particularly for diagnosis of CD11a-associated diseases (typically immune
 CC responses and inflammation such as psoriasis, Crohn's disease, rheumatoid
 CC arthritis, transplant rejection, leukaemia, etc
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
 |||
 Db 2 ASK 4

RESULT 53
 AAY20193
 ID AAY20193 standard; protein; 11 AA.
 XX

AC AAY20193;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Human beta-amyloid precursor protein mutant fragment 18.
 XX
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9845322-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 02-APR-1998; 98WO-IB000705.
 XX
 PR 10-APR-1997; 97US-0043163P.
 XX
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 PA (UYUT-) RIJKSUNIV UTRECHT.
 XX
 PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
 XX
 DR WPI; 1998-609901/51.
 DR N-PSDB; AAX75753.
 XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also for
 PT treatment and prevention with specific ribozymes or wild-type RNA.
 XX
 PS Disclosure; Fig 2; 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC used of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule

CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 1 PKR 3

RESULT 54

AAW78614

ID AAW78614 standard; peptide; 11 AA.

XX

AC AAW78614;

XX

DT 04-NOV-1998 (first entry)

XX

DE SH2 domain binding inhibiting peptide SEQ ID NO:103.

XX

KW SH2 domain; binding; inhibition; interaction; site specific;

KW signal transduction; protein tyrosine kinase; phosphotyrosine;

KW growth factor receptor; oncogene; cellular growth; cell proliferation;

KW metabolic control; diabetes; PTK; proto-oncogene; insulin receptor.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 4

FT /note= "unspecified"

XX

PN US5801149-A.

XX

PD 01-SEP-1998.

XX

PF 21-MAR-1995; 95US-00408604.

XX

PR 19-JUN-1991; 91US-00722359.

PR 09-OCT-1992; 92US-00959949.

PR 08-OCT-1993; 93US-00134558.

XX

PA (JOSL-) JOSLIN DIABETES CENT INC.

XX

PI Shoelson S;

XX

DR WPI; 1998-494822/42.

XX

PT Inhibiting site-specific SH2 domain interaction - with peptide containing

PT phosphotyrosine or phosphotyrosine mimic.

XX

PS Disclosure; Col 73; 70pp; English.

XX

CC A method has been developed of inhibiting a site-specific interaction
CC between a first molecule having an SH2 domain and a second molecule that
CC interacts with the SH2 domain. The method comprises contacting the first
CC molecule with a 4- to 30-mer peptide containing a sequence of formula: R1
CC -Met-R3-Met (I), where R1 = phosphotyrosine (pTyr) or a phosphotyrosine
CC analogue having a hydrolysis-resistant phosphorous moiety, and R3 = any
CC amino acid. AAW78501 to AAW78523 represent specifically claimed examples
CC of the peptides described. The peptides are useful for modulating both
CC cellular growth to control unwanted cell proliferation in e.g. selected
CC malignancies and for metabolic control in e.g. diabetes, by inhibiting
CC signal transduction molecules such as protein tyrosine kinases (PTKs)
CC which include growth factor receptors, proto-oncogene and oncogene
CC products and the insulin receptor. The peptides are also useful for
CC treating and for studying the enzymatic mechanisms of PTPase activity and
CC the metabolic and biochemical roles of PTPases. AAW78524 to AAW78702
CC represent other peptides given in the present invention, but which are
CC not specifically claimed

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10

|||

Db 6 NIK 8

RESULT 55

AAW62443

ID AAW62443 standard; peptide; 11 AA.

XX

AC AAW62443;

XX

DT 01-OCT-1998 (first entry)

XX

DE Human neutrophil granule bactericidal derived peptide SEQ ID NO:58.

XX

KW Bactericidal; Pseudomonas sp; endotoxin shock; bacterial infection;

KW bactericidal permeability increasing factor; B/PI; neutralising;

KW human neutrophil granule bactericidal protein.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US5786324-A.

XX

PD 28-JUL-1998.

XX

PF 24-MAR-1994; 94US-00218026.

XX

PR 24-MAR-1994; 94US-00218026.

XX

PA (MINU) UNIV MINNESOTA.

XX
 PI Mayo K, Haseman JR, Gray B;
 XX
 DR WPI; 1998-436578/37.
 XX
 PT Bactericidal and endotoxin-neutralising peptides - used in treating e.g.
 PT Pseudomonas species infection and in protectively coating prosthetic
 PT devices.
 XX
 PS Example 1; Col 19; 46pp; English.
 XX
 CC The present invention describes bactericidal peptides (BP): (a) for
 CC Pseudomonas species; (b) with endotoxin neutralising activity; (c) with
 CC both endotoxin neutralising activity and bactericidal activity for
 CC Pseudomonas aeruginosa; (d) a hybrid peptide with endotoxin neutralising
 CC activity and bactericidal activity, the peptide having at least 1 amino
 CC acid sequence of a peptide with endotoxin neutralising activity combined
 CC with at least 1 different amino acid sequence of a peptide that has
 CC bactericidal activity; and (e) a prosthetic device which has a sufficient
 CC amount of BP attached to the surface to inhibit bacterial growth. The
 CC peptides of the invention are used in treating bacterial infection such
 CC as Pseudomonas strains e.g. for P. aeruginosa at 10⁻⁷ to 10⁻⁹ M, and
 CC Escherichia coli. The peptides are also used to treat endotoxin shock.
 CC The present sequence represents a peptide derived from human neutrophil
 CC granule bactericidal protein from an example of the present invention
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
 |||
 Db 3 NIK 5

RESULT 56

AAW79785

ID AAW79785 standard; peptide; 11 AA.

XX

AC AAW79785;

XX

DT 10-DEC-1998 (first entry)

XX

DE Amino acids 300-314 of a human mutated activated protein C (APC).

XX

KW Human; activated protein C; APC; blood anticoagulant; protein C; PC;
 KW protein S; PS; inhibit; thrombosis; treat; prevent.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9844000-A1.

XX

PD 08-OCT-1998.

XX

PF 18-MAR-1998; 98WO-SE000490.
 XX
 PR 03-APR-1997; 97SE-00001228.
 XX
 PA (TACT-) TAC THROMBOSIS & COAGULATION AB.
 XX
 PI Dahlbaeck B;
 XX
 DR WPI; 1998-542633/46.
 XX
 PT New variant blood coagulation component with enhanced activity - useful
 PT to inhibit thrombosis and in the treatment of blood coagulation
 PT disorders.
 XX
 PS Claim 9; Page 47; 37pp; English.
 XX
 CC The present sequence represents a variant of amino acids 300-314 of human
 CC activated protein C (APC). This region is essential for proteolytic and
 CC amidolytic activities, and thus for anticoagulant activity. Introduction
 CC of mutations in this area could give rise to functional variants with
 CC enhanced activity. The present sequence has amino acids 303-305 and 308
 CC missing. and the substitutions E307D and A310T, compared to wild type
 CC (see AAW79784). The specification describes a new variant blood
 CC coagulation component that is substantially homologous to a wild-type
 CC blood coagulation component, capable of expressing enhanced anticoagulant
 CC activity in the protein C-anticoagulant system, and a variant of protein
 CC C (PC), APC or protein S (PS). The variants can be used to inhibit blood
 CC coagulation, particularly thrombosis, or to treat or prevent blood
 CC coagulation disorders such as thrombosis
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
 |||
 Db 8 KRN 10

RESULT 57

AAW84064

ID AAW84064 standard; peptide; 11 AA.

XX

AC AAW84064;

XX

DT 15-MAR-1999 (first entry)

XX

DE Human V3 loop HIV receptor P60/nucleolin peptide (peak 19).

XX

KW HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;

KW P60 protein; P95 protein; nucleolin; infection; therapy; diagnosis.

XX

OS Homo sapiens.

XX

PN WO9840480-A1.

XX
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-EP001409.
XX
PR 12-MAR-1997; 97US-0040969P.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Hovanessian A, Callebaut C, Krust B, Jacotot E, Muller S;
PI Briand J, Guichard G;
XX
DR WPI; 1999-034588/03.
XX
PT New isolated V3 loop HIV receptor - comprises P95/nucleolin, P40/PHAPII
PT and P30/PHAPI proteins, used to develop products for the treatment and
PT prevention of HIV infection.
XX
PS Example 9; Page 160; 267pp; English.
XX
CC This peptide was isolated from the novel V3 loop HIV receptor P60 protein
CC by endo-lysine-C digestion. Sequencing revealed identity with amino acids
CC 635-644 of human nucleolin. The V3 loop HIV receptor, identified as a
CC cell surface receptor on e.g. CD4+ T cell line CEM, consists of an
CC association of 3 proteins, named P95, P40 and P30 (see AAW84052-54), that
CC are implicated as cofactors in the process of HIV entry into cells.
CC Microsequencing of endo-lysine-C- generated peptides showed these 3
CC proteins to be nucleolin, PHAPI and PHAPII, respectively. P60 is a
CC partial degradation product of P95. The invention provides methods,
CC products and compositions for the treatment, diagnosis and prevention of
CC HIV infection
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 8 KPK 10

RESULT 58

AAAY03664

ID AAY03664 standard; peptide; 11 AA.

XX

AC AAY03664;

XX

DT 07-JUN-1999 (first entry)

XX

DE Amino acid sequence of the malaria (M) string CTL epitope Tr42/43.

XX

KW CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope;

KW cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour;

KW malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer;

KW melanoma; HIV; breast; colon; vaccination.

XX

OS Plasmodium falciparum.

XX

PN WO9856919-A2.

XX

PD 17-DEC-1998.

XX

PF 09-JUN-1998; 98WO-GB001681.

XX

PR 09-JUN-1997; 97GB-00011957.

XX

PA (ISIS-) ISIS INNOVATION LTD.

XX

PI Mcmichael AJ, Hill AVS, Gilbert SC, Schneider J, Plebanski M;

PI Hanke T, Smith GL, Blanchard T;

XX

DR WPI; 1999-070325/06.

DR N-PSDB; AAX29204.

XX

PT Generating CD8-positive T cell response to target antigen using
PT recombinant poxvirus - for treating or preventing malaria and HIV
PT infection, also epitope strings from Plasmodium and HIV.

XX

PS Claim 38; Page 18; 85pp; English.

XX

CC The invention relates to methods and reagents for generating a protective
CC CD8+ T-cell immune response against at least one target antigen. The kits
CC of the invention comprises (i) as priming composition, a source of one or
CC more CD8+ T-cell [cytotoxic T lymphocytes-(CTL)] epitopes of the target
CC antigen, plus a carrier and (ii) as boosting composition a source of CTL
CC epitopes, with at least one CTL epitope the same as used in (i), with
CC this source being a non-replicating or replication-impaired recombinant
CC poxvirus vector (PVV) plus a carrier. If the source of CTL epitopes in
CC (i) is a viral vector, then the vector in (ii) is from a different virus.
CC The kits are used to generate an immune response (prophylactic or
CC therapeutic) against pathogens or tumours, specifically against malaria
CC parasites such as P. falciparum, or HIV, and also many other bacterial,
CC viral or parasitic pathogens. The kits are also used for protective
CC response against melanoma and cancer of breast or colon, and generally
CC wherever a strong CD8+ response is protective. The boosting composition
CC may be used alone to boost a naturally primed response against malaria.
CC The specified PVV provide an excellent booster effect, better than that
CC from wild-type poxvirus, resulting in complete rather than partial
CC protection against sporozoite challenge. Also PVV are safer to use than
CC wild-type virus. Sequences AAY03661-680 represent CTL peptide epitopes of
CC the malaria (M) string

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3

|||

Db 1 ASK 3

RESULT 59

AAY42674

ID AAY42674 standard; peptide; 11 AA.

XX

AC AAY42674;

XX

DT 17-JAN-2000 (first entry)

XX

DE HHV-6 variant A derived peptide epitope.

XX

KW Human herpes virus-6; HHV-6; infection; immunological; MIEP; epitope;

KW major immediate early protein.

XX

OS Synthetic.

OS Human herpesvirus 6.

XX

PN WO9949086-A1.

XX

PD 30-SEP-1999.

XX

PF 26-MAR-1999; 99WO-US006921.

XX

PR 26-MAR-1998; 98US-0079379P.

PR 23-MAR-1999; 99US-00274938.

XX

PA (CARR/) CARRIGAN D R.

PA (KEHL/) KEHL K K.

XX

PI Carrigan DR, Kehl KK;

XX

DR WPI; 1999-601224/51.

XX

PT Methods for the rapid detection of human herpes virus 6 variants A and B

PT utilizing antibodies raised against synthetic peptides.

XX

PS Claim 9; Page 41; 58pp; English.

XX

CC The invention relates to a method for detecting human herpes virus (HHV)-
CC 6 infection that comprises contacting host cells with immunological
CC reagents specific for an epitope of HHV-6 variant A and/or B major
CC immediate early protein (MIEP). HHV-6 peptides for raising an
CC immunological reagent that binds specifically to an epitope of: (a) HHV-6
CC variant A and not B MIEP; or (b) HHV-6 variant A and B MIEP are also
CC provided. The peptides are useful as immunological reagents, e.g.
CC hyperimmune sera. Monoclonal antibodies and recombinant DNA-derived
CC single chain fragment variables (ScFv) may be useful for detecting HHV-6
CC infection when raised against specific epitopes of the HHV-6 MIEP. The
CC methods provide a rapid culture procedure having a high level of
CC sensitivity and specificity. The methods also have shortened turnaround
CC time (compared to other known methods, e.g. the isolation of the virus in
CC cell culture, the detection of virus DNA in an acellular specimen by PCR
CC or positive immunohistochemical staining) and can be easily implemented
CC by a diagnostic laboratory

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 9 KPK 11

RESULT 60

AAy81921

ID AAY81921 standard; peptide; 11 AA.

XX

AC AAY81921;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX

PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.

XX

DR WPI; 2000-342275/30.

XX

PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal
PT side.

XX

PS Example 2; Page 9; 11pp; Japanese.

XX

CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high

CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RNI 9
|||
Db 5 RNI 7

RESULT 61

AA82340

ID AA82340 standard; peptide; 11 AA.

XX

AC AA82340;

XX

DT 22-JUN-2000 (first entry)

XX

DE Humanised anti-CD11a antibody light chain CDR1 SEQ ID NO:13.

XX

KW Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;

KW antitumour; antiviral; inflammation; immunological response; LFA-1;

KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;

KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;

KW viral infection; transplant rejection; graft rejection.

XX

OS Homo sapiens.

OS Mus sp.

XX

PN US6037454-A.

XX

PD 14-MAR-2000.

XX

PF 20-NOV-1997; 97US-00974899.

XX

PR 27-NOV-1996; 96US-0031971P.

XX

PA (GETH) GENENTECH INC.

XX

PI Jardieu PM, Presta LG;

XX

DR WPI; 2000-282241/24.

XX

PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.

PT inflammation and transplant rejection, contains human heavy variable

PT region complementarity determining regions.

XX

PS Claim 4; Col 57-58; 38pp; English.

XX

CC The present invention describes a humanised anti-CD11a antibody (Ab) that

CC binds specifically to the human CD11a I-domain. The Ab has anti-

CC inflammatory, immunosuppressant, antitumour and antiviral activities. The

CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 CC involved in leucocyte adhesion associated with inflammatory and
 CC immunological responses. The Ab are used: (i) optionally when coupled to
 CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
 CC rhinitis, leukaemia, viral infections and many others, also for
 CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine
 CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
 CC sequence represents the light chain variable region CDR1 of the humanised
 CC anti-CD11a Ab
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
 |||
 Db 2 ASK 4

RESULT 62

AAY85087

ID AAY85087 standard; peptide; 11 AA.

XX

AC AAY85087;

XX

DT 06-AUG-2003 (revised)

DT 20-JUN-2000 (first entry)

XX

DE HBV surface antigen annexin binding epitope peptide #6.

XX

KW Annexin binding epitope; hepatitis B virus; hepatitis D virus; influenza;

KW benzodiazepine; binding inhibitor; cytomegalovirus; viral infection;

KW benzothiazepine.

XX

OS Hepatitis B virus.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "Biotinylated lysine"

XX

PN WO200012547-A2.

XX

PD 09-MAR-2000.

XX

PF 25-AUG-1999; 99WO-EP006231.

XX

PR 01-SEP-1998; 98EP-00870186.
PR 29-MAR-1999; 99EP-00870062.

XX

PA (INNO-) INNOGENETICS NV.

XX

PI Depla E, Moereels H, Maertens G;

XX

DR WPI; 2000-256586/22.

XX

PT New benzodiazepine and benzothiazepine derivatives, useful for treating
PT or preventing viral infection, contain peptides that include an annexin-
PT binding epitope.

XX

PS Claim 8; Page 35; 60pp; English.

XX

CC This sequence represents a peptide derived from the surface antigen of
CC hepatitis b virus, it contains an annexin binding epitope. The invention
CC relates to benzodiazepine derivatives derivatised with at least one
CC peptide containing an annexin binding epitope of an annexin binding
CC protein (e.g. the present sequence) or its fragment. Annexins are calcium
CC dependent phospholipid binding proteins. 1,4-benzodiazepines and 1,4-
CC benzothiazepines can bind to annexin V, as can the hepatitis B small
CC surface antigen. The compositions of the invention bind to cell surface
CC annexins, and inhibit the binding and entry of viruses to the cell. The
CC benzodiazepine derivatives and some related known compounds, are used to
CC treat or prevent diseases involving protein interactions with annexins,
CC particularly viral infections and specifically hepatitis B and/or D,
CC cytomegalovirus or influenza or to screen for compounds that block
CC binding between annexins and their interacting proteins. (Updated on 06-
CC AUG-2003 to correct OS field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 9 ASK 11

RESULT 63

AAAY88529

ID AAY88529 standard; peptide; 11 AA.

XX

AC AAY88529;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide D4.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
KW treatment; prosthetic nerve guide; treatment; nervous system.

XX
 OS Synthetic.
 XX
 PN WO200018801-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 23-SEP-1999; 99WO-DK000500.
 XX
 PR 29-SEP-1998; 98DK-00001232.
 PR 29-APR-1999; 99DK-00000592.
 XX
 PA (RONN/) RONN L C B.
 PA (BOCK/) BOCK E.
 PA (HOLM/) HOLM A.
 PA (OLSE/) OLSEN M.
 PA (OSTE/) OSTERGAARD S.
 PA (JENS/) JENSEN P H.
 PA (POUL/) POULSEN F M.
 PA (SORO/) SOROKA V.
 PA (RALE/) RALETS I.
 PA (BERE/) BEREZIN V.
 XX
 PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;
 XX
 DR WPI; 2000-293111/25.
 XX
 PT Compositions that bind neural cell adhesion molecules useful for treating
 PT disorders of the nervous system and muscles e.g. Alzheimer's and
 PT Parkinson's diseases.
 XX
 PS Claim 20; Page 82; 119pp; English.
 XX
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
 CC NCAM is found in three forms, two of which are transmembrane forms, while
 CC the third is attached via a lipid anchor to the cell membrane. All three
 CC NCAM forms have an extracellular structure consisting five immunoglobulin
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
 CC terminal. The present sequence represents a peptide which binds to the
 CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
 CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
 CC outgrowth from NCAM presenting cells, and is also capable of promoting
 CC the proliferation of NCAM presenting cells. The compound may be used in
 CC the treatment of normal, degenerated or damaged NCAM presenting cells.
 CC The compound may in particular be used to treat diseases of the central
 CC and peripheral nervous systems such as post operative nerve damage,
 CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
 CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
 CC dementias, sclerosis, nerve degeneration associated with diabetes
 CC mellitus, disorders affecting the circadian clock or neuro-muscular
 CC transmission and schizophrenia. Conditions affecting the muscles may also
 CC be treated with the compound, such as conditions associated with impaired
 CC function of neuromuscular connections (e.g. genetic or traumatic shock or
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
 CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
 CC liver and bowel may also be treated using the compound. The compound is

CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 9 KPK 11

RESULT 64

AAAY88563

ID AAY88563 standard; peptide; 11 AA.

XX

AC AAY88563;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Ig1 binding peptide D4 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.

XX

PS Example 5; Fig 7; 119pp; English.

XX

CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The invention relates to a compound containing a peptide which
CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,
CC and is capable of stimulating or promoting neurite outgrowth from NCAM
CC presenting cells, and is also capable of promoting the proliferation of
CC NCAM presenting cells. The present sequence represents a control peptide
CC used in the identification of those binding peptides which can be used in
CC the compound. The compound may be used in the treatment of normal,
CC degenerated or damaged NCAM presenting cells. The compound may in
CC particular be used to treat diseases of the central and peripheral
CC nervous systems such as post operative nerve damage, traumatic nerve
CC damage, impaired myelination of nerve fibres, conditions resulting from a
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
CC nerve degeneration associated with diabetes mellitus, disorders affecting
CC the circadian clock or neuro-muscular transmission and schizophrenia.
CC Conditions affecting the muscles may also be treated with the compound,
CC such as conditions associated with impaired function of neuromuscular
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
CC be treated using the compound. The compound is used in a prosthetic nerve
CC guide, and also to stimulate the ability to learn, and to stimulate the
CC memory of a subject

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 9 KPK 11

RESULT 65

AAY88560

ID AAY88560 standard; peptide; 11 AA.

XX

AC AAY88560;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Ig1 binding peptide 3Cscr used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 KW treatment; prosthetic nerve guide; treatment; nervous system.
 XX
 OS Synthetic.
 XX
 PN WO200018801-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 23-SEP-1999; 99WO-DK000500.
 XX
 PR 29-SEP-1998; 98DK-00001232.
 PR 29-APR-1999; 99DK-00000592.
 XX
 PA (RONN/) RONN L C B.
 PA (BOCK/) BOCK E.
 PA (HOLM/) HOLM A.
 PA (OLSE/) OLSEN M.
 PA (OSTE/) OSTERGAARD S.
 PA (JENS/) JENSEN P H.
 PA (POUL/) POULSEN F M.
 PA (SORO/) SOROKA V.
 PA (RALE/) RALETS I.
 PA (BERE/) BEREZIN V.
 XX
 PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;
 XX
 DR WPI; 2000-293111/25.
 XX
 PT Compositions that bind neural cell adhesion molecules useful for treating
 PT disorders of the nervous system and muscles e.g. Alzheimer's and
 PT Parkinson's diseases.
 XX
 PS Example 5; Fig 7; 119pp; English.
 XX
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
 CC NCAM is found in three forms, two of which are transmembrane forms, while
 CC the third is attached via a lipid anchor to the cell membrane. All three
 CC NCAM forms have an extracellular structure consisting five immunoglobulin
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
 CC terminal. The invention relates to a compound containing a peptide which
 CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,
 CC and is capable of stimulating or promoting neurite outgrowth from NCAM
 CC presenting cells, and is also capable of promoting the proliferation of
 CC NCAM presenting cells. The present sequence represents a control peptide
 CC used in the identification of those binding peptides which can be used in
 CC the compound. The compound may be used in the treatment of normal,
 CC degenerated or damaged NCAM presenting cells. The compound may in
 CC particular be used to treat diseases of the central and peripheral
 CC nervous systems such as post operative nerve damage, traumatic nerve
 CC damage, impaired myelination of nerve fibres, conditions resulting from a
 CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
 CC nerve degeneration associated with diabetes mellitus, disorders affecting
 CC the circadian clock or neuro-muscular transmission and schizophrenia.
 CC Conditions affecting the muscles may also be treated with the compound,

CC such as conditions associated with impaired function of neuromuscular
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
CC be treated using the compound. The compound is used in a prosthetic nerve
CC guide, and also to stimulate the ability to learn, and to stimulate the
CC memory of a subject

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11

|||

Db 8 IKA 10

RESULT 66

AAAY88538

ID AAY88538 standard; peptide; 11 AA.

XX

AC AAY88538;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide #10.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN I. C. B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P. H.

PA (POUL/) POULSEN F. M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;
 XX
 DR WPI; 2000-293111/25.
 XX
 PT Compositions that bind neural cell adhesion molecules useful for treating
 PT disorders of the nervous system and muscles e.g. Alzheimer's and
 PT Parkinson's diseases.
 XX
 PS Example 4; Page 25; 119pp; English.
 XX
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
 CC NCAM is found in three forms, two of which are transmembrane forms, while
 CC the third is attached via a lipid anchor to the cell membrane. All three
 CC NCAM forms have an extracellular structure consisting five immunoglobulin
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
 CC terminal. The present sequence represents a peptide which binds to the
 CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
 CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
 CC outgrowth from NCAM presenting cells, and is also capable of promoting
 CC the proliferation of NCAM presenting cells. The compound may be used in
 CC the treatment of normal, degenerated or damaged NCAM presenting cells.
 CC The compound may in particular be used to treat diseases of the central
 CC and peripheral nervous systems such as post operative nerve damage,
 CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
 CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
 CC dementias, sclerosis, nerve degeneration associated with diabetes
 CC mellitus, disorders affecting the circadian clock or neuro-muscular
 CC transmission and schizophrenia. Conditions affecting the muscles may also
 CC be treated with the compound, such as conditions associated with impaired
 CC function of neuromuscular connections (e.g. genetic or traumatic shock or
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
 CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
 CC liver and bowel may also be treated using the compound. The compound is
 CC used in a prosthetic nerve guide, and also to stimulate the ability to
 CC learn, and to stimulate the memory of a subject
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
 |||
 Db 2 KRN 4

RESULT 67

AAY99060

ID AAY99060 standard; peptide; 11 AA.

XX

AC AAY99060;

XX

DT 07-AUG-2000 (first entry)

XX

DE HLA class II binding antigen epitope peptide #249.

XX
 KW Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
 KW immune response; chronic viral disease; cancer; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
 KW allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;
 KW glomerulonephritis; food hypersensitivity; malaria.
 XX
 OS Clostridium tetani.
 XX
 PN WO9961916-A1.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US012066.
 XX
 PR 29-MAY-1998; 98US-0087192P.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Southwood S, Sidney J;
 XX
 DR WPI; 2000-097143/08.
 XX
 PT New compositions containing immunogenic peptide epitopes for various HLA
 PT class II DR molecules useful for inducing helper T cell response.
 XX
 PS Claim 1; Page 44; 60pp; English.
 XX
 CC The present invention relates to a new pharmaceutical composition
 CC comprising a unit dose form of a peptide, or analogue, comprising an
 CC epitope selected from those represented by peptides AAY98812-Y99339 which
 CC are derived from various antigens for various human leucocyte antigen
 CC class DR molecules, representative of the world wide population. The
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a
 CC helper T cell response. The pharmaceutical focuses the immune response
 CC towards selected determinants and could therefore be used in cases of
 CC chronic viral diseases and cancer. Examples of diseases that can be
 CC treated using the peptide containing pharmaceutical include autoimmune
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
 CC gravis), allograft rejection, allergies, lyme disease, hepatitis, post-
 CC streptococcal endocarditis or glomerulonephritis and food
 CC hypersensitivities. The peptide epitopes can be used to enhance immune
 CC responses against other immunogens administered with the peptides.
 CC Diseases which can be treated using immunogenic mixtures include prostate
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be
 CC used to make monoclonal antibodies useful as potential diagnostic or
 CC therapeutic agents. The peptides may also be useful as diagnostic
 CC reagents, for example, to determine the susceptibility of an individual
 CC to a treatment regimen. Also, the peptides may be used to predict which
 CC individuals will be at substantial risk of developing chronic infection.
 CC The selection of appropriate T and B cell epitopes should allow the
 CC development of epitope based vaccines particularly towards conserved
 CC epitopes of pathogens which are characterized by high sequence
 CC variability such as HIV, HCV and Malaria
 XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
|||
Db 6 IKA 8

RESULT 68

AAAY78451

ID AAY78451 standard; peptide; 11 AA.

XX

AC AAY78451;

XX

DT 09-MAY-2000 (first entry)

XX

DE Human growth hormone variant peptide sequence #22.

XX

KW Human growth hormone; hGH; prolactin; placental lactogen; modification;
KW mutagenesis.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US6013478-A.

XX

PD 11-JAN-2000.

XX

PF 24-JUN-1998; 98US-00104036.

XX

PR 28-OCT-1988; 88US-00264611.

PR 26-OCT-1989; 89US-00428066.

PR 27-APR-1992; 92US-00875204.

PR 13-OCT-1992; 92US-00960227.

PR 02-FEB-1994; 94US-00190723.

PR 06-JUN-1995; 95US-00483039.

PR 30-JUN-1997; 97US-00903398.

XX

PA (GETH) GENENTECH INC.

XX

PI Wells JA, Cunningham BC;

XX

DR WPI; 2000-159873/14.

XX

PT Recombinant production of variant polypeptides, e.g. growth hormone
PT variants with altered receptor specificity, using cells transformed with
PT DNA selected by scanning mutagenesis in at least one peptide domain.

XX

PS Disclosure; Col 26; 83pp; English.

XX

CC The present invention describes the production of a polypeptide variant
CC (I) comprising segment substituted and residue substituted growth
CC hormone, prolactin or placental lactogens. The method is particularly
CC used to produce variants of growth hormone (GH), prolactin or placental

CC lactogen, but may also be applied to receptors, interferons, and colony-
CC stimulating factors. A particular application is the production of human
CC GH variants with altered (decreased or increased) binding interaction
CC with the somatogenic receptor, i.e. compounds useful as human GH
CC (ant)agonists and which may have higher potency for stimulating other
CC human GH receptors, and as standards or tracers in immunoassays for human
CC GH. This method of DNA selection identifies the biologically active
CC residues in active domains, including those critical for interaction with
CC different targets. The present sequence represents a human GH variant
CC peptide sequence, which is used in the exemplification of the present
CC invention

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 7 SKK 9

RESULT 69

AAY78449

ID AAY78449 standard; peptide; 11 AA.

XX

AC AAY78449;

XX

DT 09-MAY-2000 (first entry)

XX

DE Human growth hormone variant peptide sequence #4.20.

XX

KW Human growth hormone; hGH; prolactin; placental lactogen; modification;
KW mutagenesis.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US6013478-A.

XX

PD 11-JAN-2000.

XX

PF 24-JUN-1998; 98US-00104036.

XX

PR 28-OCT-1988; 88US-00264611.

PR 26-OCT-1989; 89US-00428066.

PR 27-APR-1992; 92US-00875204.

PR 13-OCT-1992; 92US-00960227.

PR 02-FEB-1994; 94US-00190723.

PR 06-JUN-1995; 95US-00483039.

PR 30-JUN-1997; 97US-00903398.

XX

PA (GETH) GENENTECH INC.

XX

PI Wells JA, Cunningham BC;

XX

DR WPI; 2000-159873/14.

XX

PT Recombinant production of variant polypeptides, e.g. growth hormone
PT variants with altered receptor specificity, using cells transformed with
PT DNA selected by scanning mutagenesis in at least one peptide domain.

XX

PS Disclosure; Col 26; 83pp; English.

XX

CC The present invention describes the production of a polypeptide variant
CC (I) comprising segment substituted and residue substituted growth
CC hormone, prolactin or placental lactogens. The method is particularly
CC used to produce variants of growth hormone (GH), prolactin or placental
CC lactogen, but may also be applied to receptors, interferons, and colony-
CC stimulating factors. A particular application is the production of human
CC GH variants with altered (decreased or increased) binding interaction
CC with the somatogenic receptor, i.e. compounds useful as human GH
CC (ant)agonists and which may have higher potency for stimulating other
CC human GH receptors, and as standards or tracers in immunoassays for human
CC GH. This method of DNA selection identifies the biologically active
CC residues in active domains, including those critical for interaction with
CC different targets. The present sequence represents a human GH variant
CC peptide sequence, which is used in the exemplification of the present
CC invention

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4

|||

Db 7 SKK 9

RESULT 70

AA90160

ID AA90160 standard; peptide; 11 AA.

XX

AC AA90160;

XX

DT 06-AUG-2003 (revised)

DT 21-SEP-2000 (first entry)

XX

DE UPAR targeting sequence with spacers #10.

XX

KW Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;
KW adenovirus; hexon HVR5 loop; hexon HI loop; peripheral artery disease;
KW recombinant adenovirus vector; tumour; restenosis; gene therapy; asthma;
KW smooth muscle cell proliferation inhibitor; coronary artery disease;
KW obesity; neurodegenerative disease; infection; autoimmune disease; HIV;
KW thrombosis; diabetes; tropism-modified virus.

XX

OS Synthetic.

XX

PN WO200012738-A1.

XX

PD 09-MAR-2000.
 XX
 PF 27-AUG-1999; 99WO-IB001524.
 XX
 PR 27-AUG-1998; 98US-0098028P.
 XX
 PA (AVET) AVENTIS PHARMA SA.
 XX
 PI Vigne E, Dedieu J, Latta M, Yeh P, Perricaudet M;
 XX
 DR WPI; 2000-256653/22.
 XX
 PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus
 PT vectors having modified hexon HRV5 and HI loops and modified fiber
 PT proteins useful for targeted gene therapy to treat cancer or restenosis.
 XX
 PS Claim 15; Page 69; 128pp; English.
 XX
 CC This sequence represents a targeting sequence for UPAR, and is flanked by
 CC linkers. The invention relates to an adenovirus from which at least a
 CC part of the hexon HVR5 or HI loop is replaced with a binding peptide, or
 CC targeting sequence, flanked by connecting amino acid spacers, to
 CC functionally display its binding specificity at the capsid surface. The
 CC invention also relates to a recombinant adenovirus vector where a binding
 CC peptide, or targeting sequence, is connected to the C-terminus of the
 CC fiber by a connecting spacer, or linker, so as to functionally display
 CC its binding specificity at the capsid surface. The adenovirus or
 CC recombinant adenovirus vector can be used to preferentially express a
 CC gene in a target cell, especially a cell that expresses a UPAR. The
 CC targeted adenovirus vector preferably comprises a heterologous gene
 CC encoding a gene for treatment of a tumour or restenosis. The targeted
 CC adenovirus vector is useful for gene therapy treatment of a disease, and
 CC for manufacturing a medicine used in gene therapy treatment of a disease.
 CC The viruses can also be used to inhibit smooth muscle cell proliferation,
 CC to treat peripheral artery diseases, coronary artery diseases, obesity,
 CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,
 CC thrombosis, and diabetes. The viruses are particularly targeted against a
 CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses
 CC are tropism-modified without adversely impacting productivity of the
 CC vectors. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
 |||
 Db 2 SKK 4

RESULT 71
 AAY87899
 ID AAY87899 standard; protein; 11 AA.
 XX
 AC AAY87899;

XX
 DT 06-OCT-2000 (first entry)
 XX
 DE M. tuberculosis antigen TB64 N-terminal fragment.
 XX
 KW Tuberculosis; TB; antigen; vaccine; diagnosis; somatic; tuberculostatic;
 KW infection; interferon-gamma; IFN-gamma; protective immunity; therapy;
 KW delayed type hypersensitivity response; TB64.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200021983-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-DK000538.
 XX
 PR 08-OCT-1998; 98DK-00001281.
 PR 21-JAN-1999; 99US-0116673P.
 XX
 PA (STAT-) STATENS SERUM INST.
 XX
 PI Andersen P, Weldingh K, Hansen CV, Florio W, Okkels LMM;
 PI Skjot RLV, Rosenkrands I;
 XX
 DR WPI; 2000-317931/27.
 XX
 PT Novel polypeptide of somatic protein extract useful as vaccine against
 PT virulent Mycobacterium infection, isolated from cell wall, cell membrane
 PT and cytosol.
 XX
 PS Example 3a; Page 115; 126pp; English.
 XX
 CC This invention describes a novel polypeptide (PP) of somatic proteins
 CC extract (I) which have tuberculostatic activity. (I) or their subsequence
 CC has at least one of the following properties: (a) the PP induces an in
 CC vitro recall response, or an in vitro response, during primary infection
 CC with virulent Mycobacterium, determined by a release of interferon (IFN)-
 CC gamma, (b) PP induces a protective immunity, determined by vaccinating an
 CC animal with PP and an adjuvant, three times at two weeks intervals, (c)
 CC PP induces an in vitro response, or in vitro recall response, determined
 CC by release of IFN-gamma of at least 1000 pg/ml or 500 pg/ml,
 CC respectively, from Peripheral Blood Mononuclear Cells (PBMC) withdrawn
 CC from TB patients, or PPD positive individuals, 6 months after diagnosis,
 CC (d) PP induces a specific antibody response in a TB patient, as
 CC determined by enzyme linked immunosorbent assay (ELISA) technique or a
 CC western blot, (e) PP induces a positive delayed type hypersensitivity
 CC (DTH) response, determined by intradermal injection. (I) and (II) are
 CC useful in preparing a prophylactic or therapeutic medicine as a vaccine
 CC for induction of a protective or generation of an immune response in a
 CC mammal against infection with a virulent Mycobacterium. (I) and (II) are
 CC also useful as diagnostic reagent for the diagnosis of a virulent
 CC Mycobacterium infection. The vaccine of the invention induces efficient
 CC immunological memory, providing long term protection against TB. This
 CC sequence represents a Microbacterium tuberculosis TB64 antigen N-terminal
 CC fragment described in the invention
 XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 5 KPK 7

RESULT 72

AA81884

ID AA81884 standard; peptide; 11 AA.

XX

AC AA81884;

XX

DT 21-JUN-2000 (first entry)

XX

DE Yeast SAH1 protein fragment.

XX

KW Alpha-lactalbumin; protein analysis; protein mass spectrometric analysis;
KW capture reagent; protein-reactive group; enzyme; protein identification;
KW marker identification; disease marker; enzyme-deficiency disorder;
KW birth defect; lysosomal storage disease; diagnosis; SAH1.

XX

OS Saccharomyces sp.

XX

PN WO200011208-A1.

XX

PD 02-MAR-2000.

XX

PF 25-AUG-1999; 99WO-US019415.

XX

PR 25-AUG-1998; 98US-0097788P.

PR 03-SEP-1998; 98US-0099113P.

XX

PA (UNIW) UNIV WASHINGTON.

XX

PI Aebersold RH, Gelb MH, Gygi SP, Scott CR, Turecek F, Gerber SA;
PI Rist B;

XX

DR WPI; 2000-237662/20.

XX

PT Reagent for mass spectrometric analysis of proteins, e.g. for diagnosing
PT enzyme-deficiency diseases, comprises affinity label and protein-reactive
PT group attached via linker.

XX

PS Disclosure; Page 61; 116pp; English.

XX

CC This sequence represents a fragment of the yeast SAH1 protein. The
CC invention relates to reagent (I) for mass spectrometric analysis of
CC proteins comprises an affinity label (A) that binds selectively to a
CC capture reagent, attached, via a linker (L) that can be differentially
CC labelled with stable isotopes, to a protein-reactive group (PRG) that
CC reacts selectively with certain protein functional groups, or is an
CC enzyme substrate. (I) are used, particularly diagnostically, to identify

CC one or more proteins, or their functions, in a mixture. They may also be
CC used to detect relative expression levels of proteins in different
CC samples, particularly where these have been exposed to different stimuli
CC or changes in conditions, e.g. to assess effects of drugs, toxins,
CC temperature, mutations etc., and identified proteins may then serve as
CC markers for a change in state, e.g. malignancy. Particularly PRG is an
CC enzyme substrate and the method is used to detect enzyme-deficiency
CC disorders (birth defects or lysosomal storage diseases). (I) provides
CC rapid and quantitative analysis of proteins and their functions, and
CC provides selective isolation of peptide fragments or enzyme reaction
CC products. The complete protein profile of a cell or tissue can be
CC determined

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10

|||

Db 4 NIK 6

RESULT 73

AAB35570

ID AAB35570 standard; protein; 11 AA.

XX

AC AAB35570;

XX

DT 14-FEB-2001 (first entry)

XX

DE Uteroglobin fragment #5.

XX

KW Uteroglobin; immunoglobulin A mediated disease; IgA nephropathy;

KW autoimmune disorder; pulmonary inflammation; Wegener's granulomatosis;

KW Goodpasture's disease; diabetic glomerulosclerosis.

XX

OS Unidentified.

XX

PN WO200062795-A2.

XX

PD 26-OCT-2000.

XX

PF 13-APR-2000; 2000WO-US009979.

XX

PR 21-APR-1999; 99US-0130434P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Mukherjee AB, Zheng F, Zhang Z;

XX

DR WPI; 2000-687100/67.

XX

PT Use of a composition comprising uteroglobin (or a fragment, derivative,
PT mimetic or variant), for inhibiting or treating an immunoglobulin-A
PT mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and

PT pulmonary inflammation.

XX

PS Example 9; Page 35; 60pp; English.

XX

CC The present invention describes the use of uteroglobin in the diagnosis
CC and prevention of IgA mediated diseases, such as IgA nephropathy,
CC Wegener's granulomatosis, Goodpasture's disease and diabetic
CC glomerulosclerosis. This is possible as uteroglobin binds to fibronectin,
CC preventing the complexing of fibronectin with IgA and the deposition of
CC immune complexes in the kidney

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3

|||

Db 3 ASK 5

RESULT 74

AAB35573

ID AAB35573 standard; protein; 11 AA.

XX

AC AAB35573;

XX

DT 14-FEB-2001 (first entry)

XX

DE Uteroglobin fragment #8.

XX

KW Uteroglobin; immunoglobulin A mediated disease; IgA nephropathy;
KW autoimmune disorder; pulmonary inflammation; Wegener's granulomatosis;
KW Goodpasture's disease; diabetic glomerulosclerosis.

XX

OS Unidentified.

XX

PN WO200062795-A2.

XX

PD 26-OCT-2000.

XX

PF 13-APR-2000; 2000WO-US009979.

XX

PR 21-APR-1999; 99US-0130434P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Mukherjee AB, Zheng F, Zhang Z;

XX

DR WPI; 2000-687100/67.

XX

PT Use of a composition comprising uteroglobin (or a fragment, derivative,
PT mimetic or variant), for inhibiting or treating an immunoglobulin-A
PT mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and
PT pulmonary inflammation.

XX

PS Example 9; Page 35; 60pp; English.

XX

CC The present invention describes the use of uteroglobin in the diagnosis
CC and prevention of IgA mediated diseases, such as IgA nephropathy,
CC Wegener's granulomatosis, Goodpasture's disease and diabetic
CC glomerulosclerosis. This is possible as uteroglobin binds to fibronectin,
CC preventing the complexing of fibronectin with IgA and the deposition of
CC immune complexes in the kidney

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3

|||

Db 3 ASK 5

RESULT 75

AAM97950

ID AAM97950 standard; peptide; 11 AA.

XX

AC AAM97950;

XX

DT 24-JAN-2002 (first entry)

XX

DE Human peptide #1225 encoded by a SNP oligonucleotide.

XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.

XX

OS Homo sapiens.

XX

PN WO200147944-A2.

XX

PD 05-JUL-2001.

XX

PF 28-DEC-2000; 2000WO-US035498.

XX

PR 28-DEC-1999; 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach M;

XX

DR WPI; 2001-465210/50.

XX

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.

XX

PS Disclosure; Page 3936; 4143pp; English.

XX

CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5

|||

Db 5 KKP 7

Search completed: April 8, 2004, 15:39:46

Job time : 45.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds
 (without alignments)
 50.221 Million cell updates/sec

Title: US-09-787-443A-1
 Perfect score: 11
 Sequence: 1 ASKKPKRNIKA 11

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

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 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
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2	3	27.3	11	1	US-07-666-719-18	Sequence 18, Appl
3	3	27.3	11	1	US-07-842-089E-16	Sequence 16, Appl
4	3	27.3	11	1	US-07-842-089E-17	Sequence 17, Appl
5	3	27.3	11	1	US-07-603-675-8	Sequence 8, Appli
6	3	27.3	11	1	US-08-264-485-16	Sequence 16, Appl
7	3	27.3	11	1	US-08-264-485-17	Sequence 17, Appl
8	3	27.3	11	1	US-08-111-939-7	Sequence 7, Appli
9	3	27.3	11	1	US-08-116-733-1	Sequence 1, Appli
10	3	27.3	11	1	US-08-116-733-31	Sequence 31, Appl
11	3	27.3	11	1	US-08-116-733-32	Sequence 32, Appl

12	3	27.3	11	1	US-08-116-733-36	Sequence 36, Appl
13	3	27.3	11	1	US-08-116-733-37	Sequence 37, Appl
14	3	27.3	11	1	US-08-116-733-38	Sequence 38, Appl
15	3	27.3	11	1	US-08-116-733-39	Sequence 39, Appl
16	3	27.3	11	1	US-08-116-733-40	Sequence 40, Appl
17	3	27.3	11	1	US-08-116-733-41	Sequence 41, Appl
18	3	27.3	11	1	US-08-462-413-2	Sequence 2, Appli
19	3	27.3	11	1	US-08-432-694-16	Sequence 16, Appl
20	3	27.3	11	1	US-08-336-343A-23	Sequence 23, Appl
21	3	27.3	11	1	US-08-314-202-1	Sequence 1, Appli
22	3	27.3	11	1	US-08-366-953A-27	Sequence 27, Appl
23	3	27.3	11	1	US-08-218-026-58	Sequence 58, Appl
24	3	27.3	11	1	US-08-408-604A-103	Sequence 103, App
25	3	27.3	11	2	US-08-653-632-58	Sequence 58, Appl
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31	3	27.3	11	2	US-08-934-222-114	Sequence 114, App
32	3	27.3	11	2	US-08-933-402-114	Sequence 114, App
33	3	27.3	11	2	US-09-207-621-114	Sequence 114, App
34	3	27.3	11	2	US-08-350-260A-525	Sequence 525, App
35	3	27.3	11	2	US-08-564-063-26	Sequence 26, Appl
36	3	27.3	11	2	US-08-532-818-114	Sequence 114, App
37	3	27.3	11	2	US-08-182-067-4	Sequence 4, Appli
38	3	27.3	11	2	US-08-465-313-4	Sequence 4, Appli
39	3	27.3	11	3	US-08-467-902A-3	Sequence 3, Appli
40	3	27.3	11	3	US-08-974-899-13	Sequence 13, Appl
41	3	27.3	11	3	US-09-246-258-12	Sequence 12, Appl
42	3	27.3	11	3	US-09-231-797-114	Sequence 114, App
43	3	27.3	11	3	US-08-934-224-114	Sequence 114, App
44	3	27.3	11	3	US-08-933-843-114	Sequence 114, App
45	3	27.3	11	3	US-08-446-668-1	Sequence 1, Appli
46	3	27.3	11	3	US-08-934-223-114	Sequence 114, App
47	3	27.3	11	3	US-09-189-627A-22	Sequence 22, Appl
48	3	27.3	11	3	US-08-392-542-4	Sequence 4, Appli
49	3	27.3	11	3	US-08-602-999A-285	Sequence 285, App
50	3	27.3	11	3	US-08-652-877-64	Sequence 64, Appl
51	3	27.3	11	3	US-09-189-344-21	Sequence 21, Appl
52	3	27.3	11	3	US-08-647-405B-6	Sequence 6, Appli
53	3	27.3	11	3	US-09-177-249-39	Sequence 39, Appl
54	3	27.3	11	3	US-08-476-515A-64	Sequence 64, Appl
55	3	27.3	11	3	US-08-894-327-4	Sequence 4, Appli
56	3	27.3	11	3	US-09-532-106-12	Sequence 12, Appl
57	3	27.3	11	3	US-09-410-025-7	Sequence 7, Appli
58	3	27.3	11	3	US-09-413-492-114	Sequence 114, App
59	3	27.3	11	3	US-09-275-265-3	Sequence 3, Appli
60	3	27.3	11	4	US-09-025-596-7	Sequence 7, Appli
61	3	27.3	11	4	US-09-710-861-22	Sequence 22, Appl
62	3	27.3	11	4	US-09-685-027-4	Sequence 4, Appli
63	3	27.3	11	4	US-09-149-476-698	Sequence 698, App
64	3	27.3	11	4	US-09-500-124-285	Sequence 285, App
65	3	27.3	11	4	US-09-347-926-7	Sequence 7, Appli
66	3	27.3	11	4	US-09-129-112-17	Sequence 17, Appl
67	3	27.3	11	4	US-09-839-666-12	Sequence 12, Appl
68	3	27.3	11	4	US-09-839-743-16	Sequence 16, Appl

69	3	27.3	11	4	US-09-839-743-17	Sequence 17, Appl
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72	3	27.3	11	4	US-08-671-548C-74	Sequence 74, Appl
73	3	27.3	11	4	US-09-104-337A-525	Sequence 525, App
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76	3	27.3	11	4	US-09-380-836-8	Sequence 8, Appli
77	3	27.3	11	4	US-09-380-836-9	Sequence 9, Appli
78	3	27.3	11	4	US-09-941-611-3	Sequence 3, Appli
79	3	27.3	11	4	US-09-790-497A-39	Sequence 39, Appl
80	3	27.3	11	4	US-09-809-739-2	Sequence 2, Appli
81	3	27.3	11	4	US-09-454-204A-8	Sequence 8, Appli
82	3	27.3	11	4	US-09-576-824A-479	Sequence 479, App
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86	3	27.3	11	4	US-09-576-824A-483	Sequence 483, App
87	3	27.3	11	4	US-09-576-824A-484	Sequence 484, App
88	3	27.3	11	4	US-09-576-824A-560	Sequence 560, App
89	3	27.3	11	4	US-09-576-824A-561	Sequence 561, App
90	3	27.3	11	4	US-09-576-824A-562	Sequence 562, App
91	3	27.3	11	4	US-09-576-824A-563	Sequence 563, App
92	3	27.3	11	4	US-09-576-824A-564	Sequence 564, App
93	3	27.3	11	4	US-09-576-824A-565	Sequence 565, App
94	3	27.3	11	4	US-09-576-824A-566	Sequence 566, App
95	3	27.3	11	4	US-09-383-062-53	Sequence 53, Appl
96	3	27.3	11	5	PCT-US96-09473-17	Sequence 17, Appl
97	2	18.2	11	1	US-09-572-339-5	Sequence 5, Appli
98	2	18.2	11	1	US-09-572-339-7	Sequence 7, Appli
99	2	18.2	11	1	US-09-572-339-10	Sequence 10, Appl
100	2	18.2	11	1	US-09-572-339-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-416-035-8

; Sequence 8, Application US/08416035

; Patent No. 5739278

; GENERAL INFORMATION:

; APPLICANT: Daum, Gunter

; APPLICANT: Cool, Deborah E.

; APPLICANT: Fischer, Edmond H.

; TITLE OF INVENTION: Methods and Compositions for Protein

; TITLE OF INVENTION: Tyrosine Phosphatases

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/416,035
;   FILING DATE:  30-MAR-1995
;   CLASSIFICATION:  530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/059,949
;   FILING DATE:  10-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Sharkey, Richard G.
;   REGISTRATION NUMBER:  32,629
;   REFERENCE/DOCKET NUMBER:  940010.531
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (206) 622-4900
;   TELEFAX:  (206) 682-6031
;   TELEX:  3723836
;   INFORMATION FOR SEQ ID NO:  8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-416-035-8

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Query Match          36.4%;  Score 4;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.9e+02;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      1 ASKK 4
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Db      7 ASKK 10

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RESULT 2

US-07-666-719-18

; Sequence 18, Application US/07666719

; Patent No. 5247067

; GENERAL INFORMATION:

; APPLICANT: ARIMA, Terukatsu

; APPLICANT: YAMADA, Kyoko

; APPLICANT: HATANAKA, Tadashi

; APPLICANT: NAMBA, Toshihiko

; APPLICANT: TSUJI, Masao

; TITLE OF INVENTION: PEPTIDE AND ITS USE

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: US

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/07/666,719
;   FILING DATE:  19910422
;   CLASSIFICATION:  530
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Oblon, No. 5247067man F.
;   REGISTRATION NUMBER:  24,618
;   REFERENCE/DOCKET NUMBER:  363-264-0X
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (703)521-5940
;   TELEFAX:  (703)486-2347
;   TELEX:  248855 OPAT UR
;   INFORMATION FOR SEQ ID NO:  18:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  AMINO ACID
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-07-666-719-18

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Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Db      8 KKP 10

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RESULT 3
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; Sequence 16, Application US/07842089E
; Patent No. 5356875
;   GENERAL INFORMATION:
;   APPLICANT:  SARMIENTOS, PAOLO
;   APPLICANT:  DE TAXIS DU POET, PHILIPPE
;   APPLICANT:  NITTI, GIAMPAOLO
;   APPLICANT:  SCACHERI, EMANUELA
;   TITLE OF INVENTION:  ANTI-THROMBIN POLYPEPTIDES
;   NUMBER OF SEQUENCES:  59
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE:  P.C.
;   STREET:  1755 Jefferson Davis Highway, Fourth Floor
;   CITY:  Arlington
;   STATE:  Virginia
;   COUNTRY:  U.S.A.
;   ZIP:  22202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/07/842,089E

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; FILING DATE: 26-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5356875man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-265-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Hirudinaria manillensis
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..11
; OTHER INFORMATION: /note= "This sequence corresponds
; OTHER INFORMATION: to amino acids 37-47 of SEQ ID NO:1."
US-07-842-089E-16

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Db          9 KPK 11

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RESULT 4

US-07-842-089E-17

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; Sequence 17, Application US/07842089E
; Patent No. 5356875

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GENERAL INFORMATION:

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; APPLICANT: SARMIENTOS, PAOLO
; APPLICANT: DE TAXIS DU POET, PHILIPPE
; APPLICANT: NITTI, GIAMPAOLO
; APPLICANT: SCACHERI, EMANUELA
; TITLE OF INVENTION: ANTI-THROMBIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

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COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/842,089E
; FILING DATE: 26-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5356875man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-265-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Hirudinaria manillensis
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..11
; OTHER INFORMATION: /note= "This sequence corresponds
; OTHER INFORMATION: to amino acids 37-47 of SEQ ID NO:1."
US-07-842-089E-17

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Db      9 KPK 11

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RESULT 5

US-07-603-675-8

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; Sequence 8, Application US/07603675
; Patent No. 5416006
; GENERAL INFORMATION:
; APPLICANT: Blasi, Francesco
; APPLICANT: Stoppelli, Maria P
; APPLICANT: Mastronicola, Maria R
; APPLICANT: Welinder, Karen G
; APPLICANT: Correas, Isabel
; TITLE OF INVENTION: MODIFICATION OF PLASMINOGEN ACTIVATORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/603,675
; FILING DATE: 19911218
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK90/00096
; FILING DATE: 11-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 644-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: N
; FRAGMENT TYPE: internal
US-07-603-675-8

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      3 KKP 5
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Db      3 KKP 5

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RESULT 6

US-08-264-485-16

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; Sequence 16, Application US/08264485
; Patent No. 5439820
; GENERAL INFORMATION:
; APPLICANT: SARMIENTOS, PAOLO
; APPLICANT: DE TAXIS DU POET, PHILIPPE
; APPLICANT: NITTI, GIAMPAOLO
; APPLICANT: SCACHERI, EMANUELA
; TITLE OF INVENTION: ANTI-THROMBIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,485
; FILING DATE: 23-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,089
; FILING DATE: 26-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5439820man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-265-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Hirudinaria manillensis
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..11
; OTHER INFORMATION: /note= "This sequence corresponds
; OTHER INFORMATION: to amino acids 37-47 of SEQ ID NO:1."
US-08-264-485-16

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 KPK 6
      |||
Db      9 KPK 11

```

RESULT 7

US-08-264-485-17

```

; Sequence 17, Application US/08264485
; Patent No. 5439820
; GENERAL INFORMATION:
; APPLICANT: SARMIENTOS, PAOLO
; APPLICANT: DE TAXIS DU POET, PHILIPPE
; APPLICANT: NITTI, GIAMPAOLO
; APPLICANT: SCACHERI, EMANUELA
; TITLE OF INVENTION: ANTI-THROMBIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,485
; FILING DATE: 23-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,089
; FILING DATE: 26-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5439820man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-265-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Hirudinaria manillensis
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..11
; OTHER INFORMATION: /note= "This sequence corresponds
; OTHER INFORMATION: to amino acids 37-47 of SEQ ID NO:1."
US-08-264-485-17

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 KPK 6
      |||
Db      9 KPK 11

```

```

RESULT 8
US-08-111-939-7
; Sequence 7, Application US/08111939
; Patent No. 5460951
; GENERAL INFORMATION:

```

```

; APPLICANT: Kawai, Shinji
; APPLICANT: Takeshita, Sunao
; APPLICANT: Okazaki, Makoto
; APPLICANT: Amann, Egon
; TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like
; TITLE OF INVENTION: Protein and Process for its Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/111,939
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 324033/92
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 230029/92
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 02481.1321-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; DESCRIPTION: OSF 5.1 (antigen peptide)
; DESCRIPTION: segment of mouse OSF-5 from the 116th to
; DESCRIPTION: the 126th amino acid residue
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-111-939-7

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 KPK 6
      |||
Db      1 KPK 3

```

RESULT 9

US-08-116-733-1

```
; Sequence 1, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
;   APPLICANT: PALKER, Thomas J.
;   APPLICANT: HAYNES, Barton F.
;   TITLE OF INVENTION: SYNTHETIC PEPTIDES
;   NUMBER OF SEQUENCES: 46
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: NIXON & VANDERHYE P.C.
;     STREET: 1100 NORTH GLEBE ROAD
;     CITY: ARLINGTON
;     STATE: VIRGINIA
;     COUNTRY: U.S.A.
;     ZIP: 22201-4714
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/116,733
;     FILING DATE: 07-SEP-1993
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: WILSON, MARY J.
;     REGISTRATION NUMBER: 32,955
;     REFERENCE/DOCKET NUMBER: 1579-33
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (703) 816-4000
;     TELEFAX: (703) 816-4100
;     TELEX: 200797 NIXN UR
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
```

US-08-116-733-1

```
Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      3 KKP 5
      |||
Db      3 KKP 5
```

RESULT 10

US-08-116-733-31

```
; Sequence 31, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
```

```

; APPLICANT:  PALKER, Thomas J.
; APPLICANT:  HAYNES, Barton F.
; TITLE OF INVENTION:  SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES:  46
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  NIXON & VANDERHYE P.C.
;   STREET:  1100 NORTH GLEBE ROAD
;   CITY:  ARLINGTON
;   STATE:  VIRGINIA
;   COUNTRY:  U.S.A.
;   ZIP:  22201-4714
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/116,733
;   FILING DATE:  07-SEP-1993
;   CLASSIFICATION:  435
; ATTORNEY/AGENT INFORMATION:
;   NAME:  WILSON, MARY J.
;   REGISTRATION NUMBER:  32,955
;   REFERENCE/DOCKET NUMBER:  1579-33
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (703) 816-4000
;   TELEFAX:  (703) 816-4100
;   TELEX:  200797 NIXN UR
; INFORMATION FOR SEQ ID NO:  31:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  11 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-116-733-31

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      3 KKP 5
      |||
Db      3 KKP 5

```

```

RESULT 11
US-08-116-733-32
; Sequence 32, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
;   APPLICANT:  PALKER, Thomas J.
;   APPLICANT:  HAYNES, Barton F.
;   TITLE OF INVENTION:  SYNTHETIC PEPTIDES
;   NUMBER OF SEQUENCES:  46
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  NIXON & VANDERHYE P.C.
;     STREET:  1100 NORTH GLEBE ROAD

```

```

; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-32

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 KKP 5
      |||
Db      3 KKP 5

```

```

RESULT 12
US-08-116-733-36
; Sequence 36, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/116,733
;   FILING DATE:  07-SEP-1993
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  WILSON, MARY J.
;   REGISTRATION NUMBER:  32,955
;   REFERENCE/DOCKET NUMBER:  1579-33
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (703) 816-4000
;   TELEFAX:  (703) 816-4100
;   TELEX:  200797 NIXN UR
;   INFORMATION FOR SEQ ID NO:  36:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-116-733-36

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 KKP 5
            |||
Db          3 KKP 5

```

RESULT 13

US-08-116-733-37

```

; Sequence 37, Application US/08116733
; Patent No. 5516632
;   GENERAL INFORMATION:
;   APPLICANT:  PALKER, Thomas J.
;   APPLICANT:  HAYNES, Barton F.
;   TITLE OF INVENTION:  SYNTHETIC PEPTIDES
;   NUMBER OF SEQUENCES:  46
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  NIXON & VANDERHYE P.C.
;   STREET:  1100 NORTH GLEBE ROAD
;   CITY:  ARLINGTON
;   STATE:  VIRGINIA
;   COUNTRY:  U.S.A.
;   ZIP:  22201-4714
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/116,733
;   FILING DATE:  07-SEP-1993
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:

```

; NAME: WILSON, MARY J.
 ; REGISTRATION NUMBER: 32,955
 ; REFERENCE/DOCKET NUMBER: 1579-33
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4000
 ; TELEFAX: (703) 816-4100
 ; TELEX: 200797 NIXN UR
 ; INFORMATION FOR SEQ ID NO: 37:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-116-733-37

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
 |||
 Db 3 KKP 5

RESULT 14

US-08-116-733-38

; Sequence 38, Application US/08116733
 ; Patent No. 5516632
 ; GENERAL INFORMATION:
 ; APPLICANT: PALKER, Thomas J.
 ; APPLICANT: HAYNES, Barton F.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/116,733
 ; FILING DATE: 07-SEP-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WILSON, MARY J.
 ; REGISTRATION NUMBER: 32,955
 ; REFERENCE/DOCKET NUMBER: 1579-33
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4000
 ; TELEFAX: (703) 816-4100
 ; TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-38

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 3 KKP 5

RESULT 15

US-08-116-733-39

; Sequence 39, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-39

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 3 KKP 5

RESULT 16

US-08-116-733-40

; Sequence 40, Application US/08116733

; Patent No. 5516632

; GENERAL INFORMATION:

; APPLICANT: PALKER, Thomas J.

; APPLICANT: HAYNES, Barton F.

; TITLE OF INVENTION: SYNTHETIC PEPTIDES

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/116,733

; FILING DATE: 07-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 1579-33

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-116-733-40

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||

Db

3 KKP 5

RESULT 17

US-08-116-733-41

; Sequence 41, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-41

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5

|||

Db 3 KKP 5

RESULT 18

US-08-462-413-2

; Sequence 2, Application US/08462413
; Patent No. 5530009

```

; GENERAL INFORMATION:
; APPLICANT: Cho, Sung Y.
; APPLICANT: Copp, James D.
; APPLICANT: Ginah, Francis O.
; APPLICANT: Hansen, Guy J.
; APPLICANT: Hippskind, Philip A.
; APPLICANT: Huff, Bret E.
; APPLICANT: Martinelli, Michael J.
; APPLICANT: Staszak, Michael A.
; APPLICANT: Tharp-Taylor, Roger W.
; TITLE OF INVENTION: PROCESS FOR PREPARING NON-PEPTIDYL
; TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,413
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,708
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-462-413-2

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 PKR 7
      |||
Db      2 PKR 4

```

RESULT 19

US-08-432-694-16

; Sequence 16, Application US/08432694

; Patent No. 5641751

; GENERAL INFORMATION:

; APPLICANT: Heavner, George A.

; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &

; ADDRESSEE: No. 5641751ris

; STREET: One Liberty Place, 46th floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/432,694

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: DeLuca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: CCOR-0230

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-432-694-16

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3

|||

Db 2 ASK 4

RESULT 20

US-08-336-343A-23

; Sequence 23, Application US/08336343A

; Patent No. 5677144

; GENERAL INFORMATION:

; APPLICANT: Ullrich, Axel

; APPLICANT: Alves, Frauke

```

; TITLE OF INVENTION: CCK-2, A No. 5677144e1 Receptor Tyrosine Kinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,343A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-336-343A-23

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 KKP 5
      |||
Db      4 KKP 6

```

RESULT 21

US-08-314-202-1

```

; Sequence 1, Application US/08314202
; Patent No. 5702905
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Miyoko
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HUMAN VENTRICULAR
; TITLE OF INVENTION: MYOSIN LIGHT CHAINS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor

```

```

; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,202
; FILING DATE: 28-SEP-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1112-1-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE:
US-08-314-202-1

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ASK 3
      |||
Db      6 ASK 8

```

RESULT 22

```

US-08-366-953A-27
; Sequence 27, Application US/08366953A
; Patent No. 5766593
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 PEPTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1720
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,953A
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cook Ph.D., Robert R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-324
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-366-953A-27

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 NIK 10
        |||
Db      1 NIK 3

```

RESULT 23

US-08-218-026-58

```

; Sequence 58, Application US/08218026
; Patent No. 5786324
; GENERAL INFORMATION:
; APPLICANT: Gray, Beulah
; APPLICANT: Haseman, Judith R.
; APPLICANT: Mayo, Kevin
; TITLE OF INVENTION: Synthetic Peptides with Bactericidal
; TITLE OF INVENTION: Activity and Endotoxin Neutralizing Activity for Gram
; TITLE OF INVENTION: Negative Bacteria and Methods for Their Use
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5786324west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,026
; FILING DATE: 24-MAR-1994

```


; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchyk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 600.286US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-218-026-58

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
|||
Db 3 NIK 5

RESULT 24

US-08-408-604A-103
; Sequence 103, Application US/08408604A
; Patent No. 5801149
; GENERAL INFORMATION:
; APPLICANT: Shoelson, Steven
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,604A
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/134,558
; FILING DATE: 08-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,949
; FILING DATE: 09-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/722,359

```

; FILING DATE: 19-JUNE-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-014CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-408-604A-103

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 NIK 10
        |||
Db      6 NIK 8

```

RESULT 25

US-08-653-632-58

```

; Sequence 58, Application US/08653632
; Patent No. 5830860
; GENERAL INFORMATION:
; APPLICANT: GRAY, Beulah
; APPLICANT: HASEMAN, Judith R.
; APPLICANT: MAYO, Kevin
; TITLE OF INVENTION: PEPTIDES WITH BACTERICIDAL AND ENDOTOXIN NEUTRALIZING
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 5830860west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,632
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/218026
; FILING DATE: 24-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettelberger, Denise M

```

; REGISTRATION NUMBER: 33,924
; REFERENCE/DOCKET NUMBER: 600.286US11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5268
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-653-632-58

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
|||
Db 3 NIK 5

RESULT 26
US-08-669-721-21
; Sequence 21, Application US/08669721
; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-669-721-21

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 3 PKR 5

RESULT 27

US-08-856-663-8

; Sequence 8, Application US/08856663
; Patent No. 5849558
; GENERAL INFORMATION:
; APPLICANT: MORGAN, RICHARD
; APPLICANT: CHANG, ZHIYUH
; TITLE OF INVENTION: DISCOVERY OF AND
; TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE
; TITLE OF INVENTION: PSPGI RESTRICTION ENDONUCLEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: New England Biolabs, Inc.
; STREET: 32 Tozer Road
; CITY: Beverly
; STATE: MA
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,663
; FILING DATE: 15-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 978-927-5054

; TELEFAX: 978-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-856-663-8

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 2 KKP 4

RESULT 28

US-08-737-085A-12

; Sequence 12, Application US/08737085A

; Patent No. 5869232

; GENERAL INFORMATION:

; APPLICANT: SALLBERG, MATTI

; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY

; TITLE OF INVENTION: EXCHANGER

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DARBY & DARBY PC

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/737,085A

; FILING DATE: 27-DEC-1996

; CLASSIFICATION: 426

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Green, Reza

; REGISTRATION NUMBER: 38,475

; REFERENCE/DOCKET NUMBER: 3846/0C569

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-527-7659

; TELEFAX: 212-753-6237

; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-085A-12

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
|||
Db 5 KRN 7

RESULT 29

US-08-466-975A-3

; Sequence 3, Application US/08466975A
; Patent No. 5910404
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; APPLICANT: POLLET, DIRK
; APPLICANT: MAERTENS, GEERT
; APPLICANT: VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,975A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,671
; FILING DATE:
; APPLICATION NUMBER: US 07/920,286
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-975A-3

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
|||
Db 5 KRN 7

RESULT 30

US-08-391-671A-3

; Sequence 3, Application US/08391671A
; Patent No. 5922532
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; APPLICANT: POLLET, DIRK
; APPLICANT: MAERTENS, GEERT
; APPLICANT: VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,671A
; FILING DATE: 21-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/920,286
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP91/02409

```

; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-391-671A-3

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 KRN 8
      |||
Db      5 KRN 7

```

```

RESULT 31
US-08-934-222-114
; Sequence 114, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,222
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:

```


; APPLICATION NUMBER: 08/532,818
 ; FILING DATE: 03-MAY-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: U.S. 08/143,364
 ; FILING DATE: 29-OCT-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: U.S. 08/051,741
 ; FILING DATE: 23-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Isacson, John P.
 ; REGISTRATION NUMBER: 33,751
 ; REFERENCE/DOCKET NUMBER: 040433/0148
 ; INFORMATION FOR SEQ ID NO: 114:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-934-222-114

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
 |||
 Db 4 ASK 6

RESULT 32

US-08-933-402-114

; Sequence 114, Application US/08933402
 ; Patent No. 5948887
 ; GENERAL INFORMATION:
 ; APPLICANT: EVANS, Herbert J.
 ; APPLICANT: KINI, R. Manjunatha
 ; TITLE OF INVENTION: Polypeptides That Include Conformation-
 ; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
 Interaction
 ; TITLE OF INVENTION: Site
 ; NUMBER OF SEQUENCES: 153
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: Suite 500, 3000 K Street NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20007
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/933,402
 ; FILING DATE: 19-SEPT-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/532,818

```

; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-114

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ASK 3
        |||
Db      4 ASK 6

```

RESULT 33

```

US-09-207-621-114
; Sequence 114, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein
Interaction Sit
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294

```

```

; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-114

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ASK 3
        |||
Db      4 ASK 6

```

RESULT 34

```

US-08-350-260A-525
; Sequence 525, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A

```

; FILING DATE: 05-DEC-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9110549.4
 ; FILING DATE: 15-MAY-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9206318.9
 ; FILING DATE: 24-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB91/01134
 ; FILING DATE: 10-JUL-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB92/00883
 ; FILING DATE: 15-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB93/00605
 ; FILING DATE: 24-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/150,002
 ; FILING DATE: 31-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/307,619
 ; FILING DATE: 16-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W
 ; REGISTRATION NUMBER: 36,107
 ; REFERENCE/DOCKET NUMBER: 28111/32372
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; INFORMATION FOR SEQ ID NO: 525:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-350-260A-525

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
 |||
 Db 4 SKK 6

RESULT 35
 US-08-564-063-26
 ; Sequence 26, Application US/08564063
 ; Patent No. 5962418
 ; GENERAL INFORMATION:
 ; APPLICANT: SAKARIASSEN, Kjell S
 ; APPLICANT: STEPHENS, Ross W
 ; APPLICANT: ORNING, Lars
 ; TITLE OF INVENTION: FACTOR VII-DERIVED PEPTIDES
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Testa, Hurwitz & Thibault, LLP
; STREET: 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,063
; FILING DATE: 28-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, Paula A
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FRD-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-564-063-26

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 KRN 8
        |||
Db      8 KRN 10

```

RESULT 36

US-08-532-818-114

; Sequence 114, Application US/08532818

; Patent No. 5965698

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

; TITLE OF INVENTION: Site

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

```

; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-532-818-114

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ASK 3
      |||
Db      4 ASK 6

```

```

RESULT 37
US-08-182-067-4
; Sequence 4, Application US/08182067
; Patent No. 5985279
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN
; APPLICANT: CROWE, SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,067
; FILING DATE: 23-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01289
; FILING DATE: 15-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9115364.3
; FILING DATE: 16-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1786-118A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-182-067-4

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 ASK 3
        |||
Db      2 ASK 4

```

RESULT 38

US-08-465-313-4

```

; Sequence 4, Application US/08465313
; Patent No. 5997867
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN J.
; APPLICANT: CROWE, J. SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/465,313
;   FILING DATE:  05-JUN-1995
;   CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/182,067
;   FILING DATE:  23-MAR-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/GB92/01289
;   FILING DATE:  15-JUL-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  GB 9115364.3
;   FILING DATE:  16-JUL-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  BROOK, DAVID E.
;   REGISTRATION NUMBER:  22,592
;   REFERENCE/DOCKET NUMBER:  LYNX91-01A2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (617) 861-6240
;   TELEFAX:  (617) 861-9540
;   INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-465-313-4

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 ASK 3
        |||
Db      2 ASK 4

```

```

RESULT 39
US-08-467-902A-3
; Sequence 3, Application US/08467902A
; Patent No. 6007982
;   GENERAL INFORMATION:
;   APPLICANT:  DELEYS, ROBERT J
;   APPLICANT:  POLLET, DIRK
;   APPLICANT:  MAERTENS, GEERT
;   APPLICANT:  VAN HEUVERSWUN, HUGO
;   TITLE OF INVENTION:  SYNTHETIC ANTIGENS FOR THE DETECTION OF
;   TITLE OF INVENTION:  ANTIBODIES TO HEPATITIS C VIRUS
;   NUMBER OF SEQUENCES:  23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  NIXON & VANDERHYE P.C.
;   STREET:  1100 NORTH GLEBE ROAD
;   CITY:  ARLINGTON
;   STATE:  VA

```



```

; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,902A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,671
; FILING DATE:
; APPLICATION NUMBER: US 07/920,286
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-467-902A-3

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 KRN 8
      |||
Db      5 KRN 7

```

RESULT 40

US-08-974-899-13

```

; Sequence 13, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,899
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/031971
 ; FILING DATE: 11/27/96
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P1014R1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 US-08-974-899-13

Query Match 27.3%; Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
 |||
 Db 2 ASK 4

RESULT 41
 US-09-246-258-12
 ; Sequence 12, Application US/09246258
 ; Patent No. 6040137
 ; GENERAL INFORMATION:
 ; APPLICANT: SALLBERG, MATTI
 ; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
 ; TITLE OF INVENTION: EXCHANGER
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DARBY & DARBY PC
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/246,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/737,085
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/OC569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-246-258-12

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy          6 KRN 8
            |||
Db          5 KRN 7

```

RESULT 42

US-09-231-797-114

; Sequence 114, Application US/09231797

; Patent No. 6084066

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein
Interaction Sit

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,797
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-231-797-114

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ASK 3
      |||
Db      4 ASK 6

```

RESULT 43

US-08-934-224-114

; Sequence 114, Application US/08934224

; Patent No. 6100044

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

; TITLE OF INVENTION: Site

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,224
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-224-114

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ASK 3
      |||
Db      4 ASK 6

```

RESULT 44

US-08-933-843-114

; Sequence 114, Application US/08933843

; Patent No. 6111069

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction

; TITLE OF INVENTION: Site

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

```

; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,843
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-843-114

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 ASK 3
      |||
Db      4 ASK 6

```

```

RESULT 45
US-08-446-668-1
; Sequence 1, Application US/08446668
; Patent No. 6140058
; GENERAL INFORMATION:
; APPLICANT: Lane, David P.
; APPLICANT: Hupp, Theodore R.
; TITLE OF INVENTION: ACTIVATION OF P53 PROTEIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/446,668
;   FILING DATE:  24-JUL-1995
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Dreger, Walter H.
;   REGISTRATION NUMBER:  24,190
;   REFERENCE/DOCKET NUMBER:  A-61269/WHD/MTK
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-781-1989
;   TELEFAX:  415-398-3249
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  unknown
;   TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-08-446-668-1

```

```

Query Match          27.3%;  Score 3;  DB 3;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 SKK 4
      |||
Db      1 SKK 3

```

RESULT 46

US-08-934-223-114

```

; Sequence 114, Application US/08934223
; Patent No. 6147189
;   GENERAL INFORMATION:
;   APPLICANT:  EVANS, Herbert J.
;   APPLICANT:  KINI, R. Manjunatha
;   TITLE OF INVENTION:  Polypeptides That Include Conformation-
;   TITLE OF INVENTION:  Constraining Groups Which Flank A Protein-Protein
Interaction
;   TITLE OF INVENTION:  Site
;   NUMBER OF SEQUENCES:  153
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Foley & Lardner
;   STREET:  Suite 500, 3000 K Street NW
;   CITY:  Washington
;   STATE:  DC
;   COUNTRY:  USA
;   ZIP:  20007
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/934,223

```

```

; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-223-114

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ASK 3
      |||
Db      4 ASK 6

```

```

RESULT 47
US-09-189-627A-22
; Sequence 22, Application US/09189627A
; Patent No. 6159691
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas
; APPLICANT: de la Luna, Susana
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
; FILE REFERENCE: 620-54
; CURRENT APPLICATION NUMBER: US/09/189,627A
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 08/723,415
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: GB 9610195
; PRIOR FILING DATE: 1996-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DP-3 peptide
US-09-189-627A-22

```


Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 9 SKK 11

RESULT 48

US-08-392-542-4

; Sequence 4, Application US/08392542

; Patent No. 6169073

; GENERAL INFORMATION:

; APPLICANT: Halazonetis, Thanos

; APPLICANT: Hartwig, Wolfgang

; TITLE OF INVENTION: Peptides nad Peptidomimetics with

; TITLE OF INVENTION: Structural Similarity to Human p53 That Activate p53

; TITLE OF INVENTION: Function

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner, Birch, McKie & Beckett

; STREET: 1001 G Street, N.W.

; CITY: Washington, D.C.

; STATE: District of Columbia

; COUNTRY: U.S.

; ZIP: 20001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/392,542

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Posorske, Laurence H.

; REGISTRATION NUMBER: 34,698

; REFERENCE/DOCKET NUMBER: 0486.48439

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9100

; TELEFAX: 202 508-9299

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-392-542-4

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||

RESULT 49

US-08-602-999A-285

; Sequence 285, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 285:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-602-999A-285

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7

|||

Db 7 PKR 9

RESULT 50

US-08-652-877-64

; Sequence 64, Application US/08652877

; Patent No. 6187548

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalms, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd., 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.5.1

; SOFTWARE: Word 6.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,877

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15203

; FILING DATE: 22-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,314

; FILING DATE: 07-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A1355E-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-454-3816

; TELEFAX: 610-454-3808

; INFORMATION FOR SEQ ID NO: 64:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: internal
US-08-652-877-64

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 3 ASK 5

RESULT 51

US-09-189-344-21

; Sequence 21, Application US/09189344

; Patent No. 6191258

; GENERAL INFORMATION:

; APPLICANT: Lamb et al., Christopher J.

; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND

; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/189,344

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/669,721

; FILING DATE: 27-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ellison, Eldora L.

; REGISTRATION NUMBER: 39,967

; REFERENCE/DOCKET NUMBER: 07251/014001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-189-344-21

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 3 PKR 5

RESULT 52

US-08-647-405B-6

; Sequence 6, Application US/08647405B
; Patent No. 6228654
; GENERAL INFORMATION:
; APPLICANT: Chait, Brian T.
; APPLICANT: Zhao, Yingming
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES
; FILE REFERENCE: Oligosaccharides
; CURRENT APPLICATION NUMBER: US/08/647,405B
; CURRENT FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Related to
; OTHER INFORMATION: human translationally controlled tumor protein
US-08-647-405B-6

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 2 ASK 4

RESULT 53

US-09-177-249-39

; Sequence 39, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249

; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-39

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
|||
Db 4 NIK 6

RESULT 54

US-08-476-515A-64

; Sequence 64, Application US/08476515A

; Patent No. 6239270

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalms, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 84

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Martin Savitzky

; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;

; STREET: 3C43,

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Compaq PC

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Word 7.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/476,515A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE94/00483

```

; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-476-515A-64

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ASK 3
        |||
Db      3 ASK 5

```

```

RESULT 55
US-08-894-327-4
; Sequence 4, Application US/08894327
; Patent No. 6245886
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
; APPLICANT: Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; TITLE OF INVENTION: function
; FILE REFERENCE: 2973.19998
; CURRENT APPLICATION NUMBER: US/08/894,327
; CURRENT FILING DATE: 1997-12-04
; EARLIER APPLICATION NUMBER: pctus96/01535
; EARLIER FILING DATE: 1996-02-16
; EARLIER APPLICATION NUMBER: 08/392,542
; EARLIER FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-894-327-4

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;

```

Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 9 SKK 11

RESULT 56

US-09-532-106-12

; Sequence 12, Application US/09532106

; Patent No. 6245895

; GENERAL INFORMATION:

; APPLICANT: SALLBERG, MATTI

; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY

; EXCHANGER

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DARBY & DARBY PC

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/532,106

; FILING DATE: 21-Mar-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/737,085A

; FILING DATE: 27-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Green, Reza

; REGISTRATION NUMBER: 38,475

; REFERENCE/DOCKET NUMBER: 3846/0C569

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-527-7659

; TELEFAX: 212-753-6237

; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-532-106-12

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8
 |||
Db 5 KRN 7

RESULT 57

US-09-410-025-7

; Sequence 7, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-7

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RNI 9
 |||
Db 5 RNI 7

RESULT 58

US-09-413-492-114

; Sequence 114, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-413-492-114

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 ASK 3
      |||
Db      4 ASK 6

```

RESULT 59

US-09-275-265-3

```

; Sequence 3, Application US/09275265
; Patent No. 6287761
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; APPLICANT: POLLET, DIRK
; APPLICANT: MAERTENS, GEERT
; APPLICANT: VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,265
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,671
; FILING DATE: 21-FEB-1995
; APPLICATION NUMBER: US 07/920,286
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-275-265-3

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Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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QY      6 KRN 8
      |||
Db      5 KRN 7

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RESULT 60
US-09-025-596-7
; Sequence 7, Application US/09025596
; Patent No. 6340463
; GENERAL INFORMATION:
; APPLICANT: Mitchell, William M.
; APPLICANT: Stratton, Charles W.
; TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: VDB98-01
; CURRENT APPLICATION NUMBER: US/09/025,596
; CURRENT FILING DATE: 1998-02-18

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; EARLIER APPLICATION NUMBER: 08/911,593
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 60/023,921
; EARLIER FILING DATE: 1996-08-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-025-596-7

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 4 KKP 6

RESULT 61

US-09-710-861-22

; Sequence 22, Application US/09710861
; Patent No. 6387649
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas
; APPLICANT: de la Luna, Susana
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
; FILE REFERENCE: 620-54
; CURRENT APPLICATION NUMBER: US/09/710,861
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US/09/189,627
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 08/723,415
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: GB 9610195
; PRIOR FILING DATE: 1996-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DP-3 peptide
US-09-710-861-22

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 9 SKK 11

RESULT 62

US-09-685-027-4

; Sequence 4, Application US/09685027

; Patent No. 6420118

; GENERAL INFORMATION:

; APPLICANT: Halazonetis, Thanos

; Hartwig, Wolfgang

; TITLE OF INVENTION: Peptides nad Peptidomimetics with

; Structural Similarity to Human p53 That Activate

p53

; Function

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner, Birch, McKie & Beckett

; STREET: 1001 G Street, N.W.

; CITY: Washington, D.C.

; STATE: District of Columbia

; COUNTRY: U.S.

; ZIP: 20001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/685,027

; FILING DATE: 10-Oct-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/392,542

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Posorske, Laurence H.

; REGISTRATION NUMBER: 34,698

; REFERENCE/DOCKET NUMBER: 0486.48439

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9100

; TELEFAX: 202 508-9299

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-685-027-4

Query Match 27.3%; Score 3; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4

|||

Db 9 SKK 11

RESULT 63

US-09-149-476-698

; Sequence 698, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11


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; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      9 IKA 11
        |||
Db      5 IKA 7
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RESULT 64

US-09-500-124-285

; Sequence 285, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/500,124
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/602,999
 ; FILING DATE: 16-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 285:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 US-09-500-124-285

Query Match 27.3%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
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 Db 7 PKR 9

RESULT 65
 US-09-347-926-7
 ; Sequence 7, Application US/09347926
 ; Patent No. 6440386
 ; GENERAL INFORMATION:
 ; APPLICANT: LEUNG, SHUI-ON
 ; TITLE OF INVENTION: STABILIZED RADIOPHOSPHATE-LABELED PROTEINS
 ; FILE REFERENCE: 018733/0936
 ; CURRENT APPLICATION NUMBER: US/09/347,926
 ; CURRENT FILING DATE: 1999-07-06
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 11
 ; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-347-926-7

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 3 ASK 5

RESULT 66

US-09-129-112-17
; Sequence 17, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Lotus japonicus
US-09-129-112-17

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
|||
Db 3 IKA 5

RESULT 67

US-09-839-666-12
; Sequence 12, Application US/09839666
; Patent No. 6469143
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; EXCHANGER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York

```

;          COUNTRY: USA
;          ZIP: 10022
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Diskette
;          COMPUTER: IBM Compatible
;          OPERATING SYSTEM: DOS
;          SOFTWARE: FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/839,666
;          FILING DATE: 19-Apr-2001
;          CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/737,085
;          FILING DATE: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Green, Reza
;          REGISTRATION NUMBER: 38,475
;          REFERENCE/DOCKET NUMBER: 3846/0C569
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 212-527-7659
;          TELEFAX: 212-753-6237
;          TELEX: 236687
;    INFORMATION FOR SEQ ID NO: 12:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 11 amino acids
;        TYPE: amino acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-839-666-12

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Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

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Qy          6 KRN 8
            |||
Db          5 KRN 7

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RESULT 68
US-09-839-743-16
; Sequence 16, Application US/09839743
; Patent No. 6472211
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. 6472211el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21

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; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-16

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 2 PKR 4

RESULT 69

US-09-839-743-17

; Sequence 17, Application US/09839743
; Patent No. 6472211
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. 6472211el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-17

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 2 PKR 4

RESULT 70

US-09-839-743-18

```
; Sequence 18, Application US/09839743
; Patent No. 6472211
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. 6472211el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Nicotiana tabacum
US-09-839-743-18
```

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Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
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QY          5 PKR 7
            |||
Db          2 PKR 4
```

RESULT 71

US-09-839-743-24

```
; Sequence 24, Application US/09839743
; Patent No. 6472211
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. 6472211el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
```

; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-24

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 3 PKR 5

RESULT 72

US-08-671-548C-74

; Sequence 74, Application US/08671548C
; Patent No. 6486130
; GENERAL INFORMATION:
; APPLICANT: LIVEY, Ian
; APPLICANT: CROWE, Brian
; APPLICANT: DORNER, Friedrich
; TITLE OF INVENTION: IMMUNOGENIC FORMULATION OF OSPC ANTIGEN VACCINE FOR THE
PREVENTION AND
; TITLE OF INVENTION: TREATMENT OF LYME DISEASE AND RECOMBINANT METHODS FOR
THE PREPARATION OF SUCH
; TITLE OF INVENTION: ANTIGENS
; FILE REFERENCE: 37974-0023
; CURRENT APPLICATION NUMBER: US/08/671,548C
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 08/284,667
; PRIOR FILING DATE: 1994-08-19
; PRIOR APPLICATION NUMBER: 08/053,863
; PRIOR FILING DATE: 1993-04-29
; PRIOR APPLICATION NUMBER: PCT/EP94/01365
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Borrelia sp.
US-08-671-548C-74

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 9 KKP 11

RESULT 73

US-09-104-337A-525

; Sequence 525, Application US/09104337A

; Patent No. 6492160

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs

; NUMBER OF SEQUENCES: 600

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; INFORMATION FOR SEQ ID NO: 525:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 525:
US-09-104-337A-525

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 4 SKK 6

RESULT 74

US-09-266-764-17
; Sequence 17, Application US/09266764
; Patent No. 6545139
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; TITLE OF INVENTION: Compositions and Methods For the Treatment and
; TITLE OF INVENTION: Prevention of Metastatic Disorders
; FILE REFERENCE: 00A146.0122
; CURRENT APPLICATION NUMBER: US/09/266,764
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/077,934
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-266-764-17

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 8 KKP 10

RESULT 75

US-09-380-836-7
; Sequence 7, Application US/09380836
; Patent No. 6551775
; GENERAL INFORMATION:
; APPLICANT: Lifton, Richard P.
; APPLICANT: Chang, Sue S.
; APPLICANT: Rossier, Bernard C.
; TITLE OF INVENTION: Method to Diagnose and Treat Pathological Conditions
; TITLE OF INVENTION: Resulting from Deficient Ion Transport such as
; TITLE OF INVENTION: Pseudohypoaldosteronism Type-1
; FILE REFERENCE: 44574-5018-US
; CURRENT APPLICATION NUMBER: US/09/380,836
; CURRENT FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/040,171
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US98/04681
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Segment of beta ENaC protein
US-09-380-836-7

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
|||
Db 9 PKR 11

Search completed: April 8, 2004, 15:52:05
Job time : 13.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds
 (without alignments)
 122.816 Million cell updates/sec

Title: US-09-787-443A-1
 Perfect score: 11
 Sequence: 1 ASKKPKRNIKA 11

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11
 Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR_78:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query			ID	Description
	Score	Match	Length	DB			
1	3	27.3	11	2	S42449	ant1 protein - pha	
2	3	27.3	11	2	B41835	translation elonga	
3	3	27.3	11	2	S19775	wound-induced prot	
4	2	18.2	11	1	XASNBA	bradykinin-potenti	
5	2	18.2	11	1	SPHO	substance P - hors	
6	2	18.2	11	1	EOOCC	eledoisin - curled	
7	2	18.2	11	1	A60654	substance P - guin	
8	2	18.2	11	1	EOOC	eledoisin - musky	
9	2	18.2	11	2	S32575	ribosomal protein	
10	2	18.2	11	2	A38841	rhodopsin homolog	
11	2	18.2	11	2	C53652	rhlR protein - Pse	
12	2	18.2	11	2	A26930	ermG leader peptid	
13	2	18.2	11	2	YHRT	morphogenetic neur	

14	2	18.2	11	2	YHHU	morphogenetic neur
15	2	18.2	11	2	YHBO	morphogenetic neur
16	2	18.2	11	2	YHXAE	morphogenetic neur
17	2	18.2	11	2	YHJFHY	morphogenetic neur
18	2	18.2	11	2	B26744	megascalikinin -
19	2	18.2	11	2	S23308	substance P - rain
20	2	18.2	11	2	S23306	substance P - Atla
21	2	18.2	11	2	A61033	ranatachykinin A -
22	2	18.2	11	2	D61033	ranatachykinin D -
23	2	18.2	11	2	JQ0395	hypothetical prote
24	2	18.2	11	2	PQ0231	beta-glucosidase (
25	2	18.2	11	2	S66606	quinoline 2-oxidor
26	2	18.2	11	2	S42587	celF protein - Esc
27	2	18.2	11	2	S33782	acetolactate synth
28	2	18.2	11	2	PC2372	58K heat shock pro
29	2	18.2	11	2	S33519	probable secreted
30	2	18.2	11	2	PT0081	protein QA300023 -
31	2	18.2	11	2	G61497	seed protein ws-23
32	2	18.2	11	2	PC4267	ribosomal protein
33	2	18.2	11	2	PQ0731	unidentified 5.7/3
34	2	18.2	11	2	A34135	DNA-binding protei
35	2	18.2	11	2	S33300	probable substance
36	2	18.2	11	2	D42965	talin - chicken (f
37	2	18.2	11	2	I54193	Rhesus blood group
38	2	18.2	11	2	S57575	T cell receptor V-
39	2	18.2	11	2	S68637	acetylcholinestera
40	2	18.2	11	2	S78765	ribosomal protein
41	2	18.2	11	2	S54347	tubulin beta chain
42	2	18.2	11	2	PN0044	protein kinase C i
43	2	18.2	11	2	PT0217	T-cell receptor be
44	2	18.2	11	2	C38887	T-cell receptor ga
45	2	18.2	11	2	I41946	T-cell receptor ga
46	2	18.2	11	2	PD0441	translation elonga
47	2	18.2	11	2	S65377	cytochrome-c oxida
48	2	18.2	11	2	S78422	ribosomal protein
49	2	18.2	11	2	PH0939	T-cell receptor be
50	2	18.2	11	2	PH0940	T-cell receptor be
51	2	18.2	11	2	PH0941	T-cell receptor be
52	2	18.2	11	2	PH0929	T-cell receptor be
53	2	18.2	11	2	PH0891	T-cell receptor be
54	2	18.2	11	2	PH0938	T-cell receptor be
55	2	18.2	11	2	PH0947	T-cell receptor be
56	2	18.2	11	2	PH0903	T-cell receptor be
57	2	18.2	11	2	PH0904	T-cell receptor be
58	2	18.2	11	2	PH0924	T-cell receptor be
59	2	18.2	11	2	PH0919	T-cell receptor be
60	2	18.2	11	2	PH0914	T-cell receptor be
61	2	18.2	11	2	PH0922	T-cell receptor be
62	2	18.2	11	2	PH0906	T-cell receptor be
63	2	18.2	11	2	A61575	Trimeresurus serin
64	2	18.2	11	2	S60294	tubulin 2 beta-3 c
65	2	18.2	11	4	PC2390	trichorozin I - fu
66	2	18.2	11	4	PC2392	trichorozin III -
67	2	18.2	11	4	S52252	hypothetical prote
68	2	18.2	11	4	I54081	retinoic acid rece
69	1	9.1	11	1	XAVIBH	bradykinin-potenti
70	1	9.1	11	1	ECLQ2M	tachykinin II - mi

71	1	9.1	11	1	GMROL	leucosulfakinin -
72	1	9.1	11	1	LFTWWE	probable trpEG lea
73	1	9.1	11	2	S66196	alcohol dehydrogen
74	1	9.1	11	2	G42762	proteasome endopep
75	1	9.1	11	2	A33917	dihydroorotase (EC
76	1	9.1	11	2	B49164	chromogranin-B - r
77	1	9.1	11	2	JN0023	substance P - chic
78	1	9.1	11	2	A40693	transgelin - sheep
79	1	9.1	11	2	PQ0682	photosystem I 17.5
80	1	9.1	11	2	S00616	parasporal crystal
81	1	9.1	11	2	S09074	cytochrome P450-4b
82	1	9.1	11	2	A57458	gene Gax protein -
83	1	9.1	11	2	D60409	kassinin-like pept
84	1	9.1	11	2	F60409	substance P-like p
85	1	9.1	11	2	E60409	substance P-like p
86	1	9.1	11	2	A61365	phyllokinin - Rohd
87	1	9.1	11	2	B60409	kassinin-like pept
88	1	9.1	11	2	C60409	kassinin-like pept
89	1	9.1	11	2	S07203	uperolein - frog (
90	1	9.1	11	2	S07207	Crinia-angiotensin
91	1	9.1	11	2	S07201	physalaemin - frog
92	1	9.1	11	2	B58501	24K kidney and bla
93	1	9.1	11	2	D58502	27K bile and gallb
94	1	9.1	11	2	A58502	38K kidney stone p
95	1	9.1	11	2	C58501	42K bile stone pro
96	1	9.1	11	2	F58501	43.5K bile stone p
97	1	9.1	11	2	S58244	pyrroloquinoline q
98	1	9.1	11	2	S04875	nifS protein - Bra
99	1	9.1	11	2	I41138	acetyl ornithine d
100	1	9.1	11	2	S35490	type II site-speci

ALIGNMENTS

RESULT 1

S42449

ant1 protein - phage P7

C;Species: phage P7

C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999

C;Accession: S42449

R;Citron, M.; Schuster, H.

Cell 62, 591-598, 1990

A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.

A;Reference number: S42448; MUID:90335968; PMID:1696181

A;Accession: S42449

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-11 <CIT>

A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5

|||

Db 2 KKP 4

RESULT 2

B41835

translation elongation factor EF-G homolog - *Bacillus subtilis* (fragment)

C;Species: *Bacillus subtilis*

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Dec-1997

C;Accession: B41835

R;Mitchell, C.; Morris, P.W.; Vary, J.C.

J. Bacteriol. 174, 2474-2477, 1992

A;Title: Identification of proteins phosphorylated by ATP during sporulation of *Bacillus subtilis*.

A;Reference number: A41835; MUID:92210489; PMID:1556067

A;Accession: B41835

A;Molecule type: protein

A;Residues: 1-11 <MIT>

A;Note: this protein is phosphorylated during stationary phase but not during exponential growth

C;Keywords: phosphoprotein

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RNI 9

|||

Db 7 RNI 9

RESULT 3

S19775

wound-induced protein - tomato (fragment)

C;Species: *Lycopersicon esculentum* (tomato)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997

C;Accession: S19775

R;Parsons, B.L.

submitted to the EMBL Data Library, May 1991

A;Reference number: S19773

A;Accession: S19775

A;Molecule type: mRNA

A;Residues: 1-11 <PAR>

A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4

|||

Db 4 SKK 6

RESULT 4

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: *Agkistrodon blomhoffi* (mamushi)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C;Accession: A01254
R;Kato, H.; Suzuki, T.
Proc. Jpn. Acad. 46, 176-181, 1970
A;Reference number: A01254
A;Accession: A01254
A;Molecule type: protein
A;Residues: 1-11 <KAT>
A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
||
Db 7 PK 8

RESULT 5

SPHO
substance P - horse
C;Species: Equus caballus (domestic horse)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C;Accession: A01558
R;Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.
A;Reference number: A01558
A;Accession: A01558
A;Molecule type: protein
A;Residues: 1-11 <STU>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
||
Db 2 PK 3

RESULT 6

EOOCC
eledoisin - curled octopus
C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
C;Accession: B01561; A01561
R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963
A;Title: The isolation and amino acid sequence of eledoisin, the active
endecapeptide of the posterior salivary glands of Eledone.
A;Reference number: A01561
A;Accession: B01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;
secretagogue; vasodilator; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
||
Db 3 SK 4

RESULT 7

A60654
substance P - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995
C;Accession: A60654
R;Murphy, R.
Neuropeptides 14, 105-110, 1989
A;Title: Primary amino acid sequence of guinea-pig substance P.
A;Reference number: A60654; MUID:90044685; PMID:2478925
A;Accession: A60654
A;Molecule type: protein
A;Residues: 1-11 <MUR>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
||
Db 2 PK 3

RESULT 8

EEOC
eledoisin - musky octopus
C;Species: Eledone moschata, Ozaena moschata (musky octopus)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998
C;Accession: A01561
R;Anastasi, A.; Erspamer, V.
Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active
endecapeptide of the posterior salivary glands of Eledone..
A;Reference number: A01561
A;Accession: A01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;
secretagogue; vasodilator; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
||
Db 3 SK 4

RESULT 9

S32575
ribosomal protein S2, plastid - squawroot plastid (fragment)
C;Species: plastid *Conopholis americana* (squawroot)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999
C;Accession: S32575
R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.
Curr. Genet. 20, 515-518, 1991
A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of
photosynthesis in a lineage of parasitic plants.
A;Reference number: S32575; MUID:92145776; PMID:1723664
A;Accession: S32575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <TAY>
A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276
C;Genetics:
A;Gene: rps2
A;Genome: plastid
C;Superfamily: *Escherichia coli* ribosomal protein S2
C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
||
Db 7 NI 8

RESULT 10

A38841
rhodopsin homolog - squid (*Watasenia scintillans*) (fragment)
N;Alternate names: visual pigment protein
C;Species: *Watasenia scintillans* (sparkling enope)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Oct-1997
C;Accession: A38841
R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.
Biochim. Biophys. Acta 957, 318-321, 1988
A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.
A;Reference number: PT0063; MUID:89051045; PMID:3191148
A;Accession: A38841
A;Molecule type: protein
A;Residues: 1-11 <SEI>
C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; retinal
F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 4 AS 5

RESULT 11

C53652
rhlR protein - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998
C;Accession: C53652
R;Ochsner, U.A.; Fiechter, A.; Reiser, J.
J. Biol. Chem. 269, 19787-19795, 1994
A;Title: Isolation, characterization, and expression in Escherichia coli of the Pseudomonas aeruginosa rhlAB genes encoding a rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis.
A;Reference number: A53652; MUID:94327521; PMID:8051059
A;Accession: C53652
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <OCH>
A;Cross-references: GB:L28170
C;Superfamily: sdiA regulatory protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RN 8
||
Db 2 RN 3

RESULT 12

A26930
ermG leader peptide 1 - Bacillus sphaericus
C;Species: Bacillus sphaericus
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 24-Sep-1999
C;Accession: A26930

R;Monod, M.; Mohan, S.; Dubnau, D.
J. Bacteriol. 169, 340-350, 1987
A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin
B resistance element from Bacillus sphaericus.
A;Reference number: A91840; MUID:87083389; PMID:3025178
A;Accession: A26930
A;Molecule type: DNA
A;Residues: 1-11 <MON>
A;Cross-references: GB:M15332; NID:g142881; PIDN:AAA22417.1; PID:g142882
C;Superfamily: unassigned leader peptides

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
||
Db 5 SK 6

RESULT 13

YHRT

morphogenetic neuropeptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator,
from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical
structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was
called head activator by the authors, because it induced head-specific growth
and differentiation in this animal. It has been found in mammalian intestine and
hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide;
pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
||
Db 6 SK 7

RESULT 14

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.1e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3

||

Db 6 SK 7

RESULT 15

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: C01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: C01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3

||

Db 6 SK 7

RESULT 16

YHXA

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
||
Db 6 SK 7

RESULT 17

YHJFHY

morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator

C;Species: Hydra attenuata

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: B93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.1e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
||
Db 6 SK 7

RESULT 18

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: Megascolia flavifrons (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp Megascolia flavifrons.

A;Reference number: A94322; MUID:87293024; PMID:3617088
A;Accession: B26744
A;Molecule type: protein
A;Residues: 1-11 <YAS>
R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.
Toxicon 26, 34, 1988
A;Title: Two kinins isolated from the venom of *Megascolia flavifrons*.
A;Reference number: A28609
A;Accession: A28609
A;Molecule type: protein
A;Residues: 1-11 <NAK>
C;Superfamily: unassigned animal peptides
C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KA 11
||
Db 10 KA 11.

RESULT 19

S23308

substance P - rainbow trout

C;Species: *Oncorhynchus mykiss* (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 1 KP 2

RESULT 20

S23306

substance P - Atlantic cod

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23306

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.1e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5

||

Db 1 KP 2

RESULT 21

A61033

ranatachykinin A - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: A61033; JE0426

R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: A61033

A;Accession: A61033

A;Molecule type: protein

A;Residues: 1-11 <KAN>

R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: JE0426; MUID:91254337; PMID:2043143

A;Accession: JE0426

A;Molecule type: protein

A;Residues: 1-11 <KOZ>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 1 KP 2

RESULT 22

D61033

ranatachykinin D - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: D61033; JE0429

R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: A61033

A;Accession: D61033

A;Molecule type: protein

A;Residues: 1-11 <KAN>

R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: JE0426; MUID:91254337; PMID:2043143

A;Accession: JE0429

A;Molecule type: protein

A;Residues: 1-11 <KOZ>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 1 KP 2

RESULT 23

JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans

N;Alternate names: hypothetical 1.4K protein

C;Species: Azorhizobium caulinodans

A;Note: host Sesbania rostrata

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Feb-1994

C;Accession: JQ0395

R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.

Mol. Gen. Genet. 219, 289-298, 1989

A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans: nucleotide sequence and plant-inducible expression.

A;Reference number: JQ0393; MUID:90136519; PMID:2615763
A;Accession: JQ0395
A;Molecule type: DNA
A;Residues: 1-11 <GOE>
A;Cross-references: GB:L18897
A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KK 4
||
Db 6 KK 7

RESULT 24

PQ0231

beta-glucosidase (EC 3.2.1.21) - Cellvibrio gilvus (fragment)

C;Species: Cellvibrio gilvus

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 07-May-1999

C;Accession: PQ0231

R;Kashiwagi, Y.; Iijima, C.; Sasaki, T.; Taniguchi, H.

Agric. Biol. Chem. 55, 2553-2559, 1991

A;Title: Characterization of a beta-glucosidase encoded by a gene from Cellvibrio gilvus.

A;Reference number: PQ0231; MUID:92144103; PMID:1368758

A;Accession: PQ0231

A;Molecule type: protein

A;Residues: 1-11 <KAS>

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 10 KP 11

RESULT 25

S66606

quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)

C;Species: Comamonas testosteroni

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66606

R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.

Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66606

A;Molecule type: protein

A;Residues: 1-11 <SCH>

A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 9 KP 10

RESULT 26

S42587

celF protein - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995

C;Accession: S42587

R;Guzzo, A.; DuBow, M.S.

Mol. Gen. Genet. 242, 455-460, 1994

A;Title: A luxAB transcriptional fusion to the cryptic celF gene of Escherichia coli displays increased luminescence in the presence of nickel.

A;Reference number: S42587; MUID:94166755; PMID:8121401

A;Accession: S42587

A;Molecule type: DNA

A;Residues: 1-11 <GUZ>

C;Genetics:

A;Gene: celF

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RN 8
||
Db 2 RN 3

RESULT 27

S33782

acetolactate synthase (EC 4.1.3.18) small chain, valine-sensitive - Serratia marcescens (fragment)

C;Species: Serratia marcescens

C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C;Accession: S33782

R;Yang, J.H.; Kim, S.S.

Biochim. Biophys. Acta 1157, 178-184, 1993

A;Title: Purification and characterization of the valine sensitive acetolactate synthase from Serratia marcescens ATCC 25419.

A;Reference number: S33781; MUID:93283409; PMID:8507653

A;Accession: S33782

A;Molecule type: protein

A;Residues: 1-11 <YAN>

A;Experimental source: ATCC 25419

C;Complex: heterotetramer; two small and two large chains

C;Function:

A;Description: catalyzes the condensation of pyruvate and alpha-ketobutyrate to form alpha-aceto-alpha-hydroxybutyrate

A;Pathway: valine, leucine, and isoleucine biosynthesis

A;Note: this isoenzyme exhibits homotropic allosterism with pyruvate
C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase;
flavoprotein; heterotetramer; magnesium; oxo-acid-lyase; valine inhibition

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RN 8
||
Db 6 RN 7

RESULT 28

PC2372

58K heat shock protein groEL [similarity] - *Bacillus cereus* (strain ts-4)
(fragment)

C;Species: *Bacillus cereus*

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C;Accession: PC2372

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation in *Bacillus cereus*.

A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2372

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <MAS>

C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IK 10
||
Db 4 IK 5

RESULT 29

S33519

probable secreted protein - *Acholeplasma laidlawii* (fragment)

C;Species: *Acholeplasma laidlawii*

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999

C;Accession: S33519

R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.

submitted to the EMBL Data Library, June 1993

A;Description: Sequence regions from *Acholeplasma laidlawii* which restore export of beta-lactamase in *Escherichia coli*.

A;Reference number: S33518

A;Accession: S33519

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <BOY>

A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KK 4
||
Db 2 KK 3

RESULT 30

PT0081

protein QA300023 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 24-Nov-1999

C;Accession: PT0081

R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.

submitted to JIPID, December 1995

A;Description: Two dimensional electrophoresis of plant proteins and
standardization of the gel patterns.

A;Reference number: PN0173

A;Accession: PT0081

A;Molecule type: protein

A;Residues: 1-11 <TSU>

A;Experimental source: Leaf

C;Keywords: acetylated amino end

F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
||
Db 1 SK 2

RESULT 31

G61497

seed protein ws-23 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: G61497

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A;Title: Microsequence analysis of winged bean seed proteins electroblotted from
two-dimensional gel.

A;Reference number: A61491; MUID:89351606; PMID:2765119

A;Accession: G61497

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HIR>

C;Keywords: glycoprotein; seed

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
 ||
Db 3 SK 4

RESULT 32

PC4267

ribosomal protein L12.1 - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997

C;Accession: PC4267

R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.

submitted to JIPID, April 1997

A;Reference number: PC4267

A;Accession: PC4267

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: strain Japonica Nihonbare

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
 ||
Db 7 PK 8

RESULT 33

PQ0731

unidentified 5.7/35K protein [imported] - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C;Accession: PQ0731

R;Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensional electrophoresis.

A;Reference number: PQ0696

A;Accession: PQ0731

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <KOM>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
 ||
Db 6 PK 7

RESULT 34

A34135

DNA-binding protein p - Crithidia fasciculata mitochondrion (fragment)

C;Species: mitochondrion Crithidia fasciculata
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999
C;Accession: A34135
R;Tittawella, I.
FEBS Lett. 260, 57-61, 1990
A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata.
A;Reference number: A34135
A;Accession: A34135
A;Molecule type: protein
A;Residues: 1-11 <TIT>
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KA 11
||
Db 9 KA 10

RESULT 35

S33300

probable substance P - smaller spotted catshark

C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999

C;Accession: S33300

R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A;Title: Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, Scyliorhinus canicula.

A;Reference number: S33300; MUID:93292508; PMID:7685693

A;Accession: S33300

A;Molecule type: protein

A;Residues: 1-11 <WAU>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 1 KP 2

RESULT 36

D42965

talín - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C;Accession: D42965

R;Hagmann, J.; Grob, M.; Burger, M.M.

J. Biol. Chem. 267, 14424-14428, 1992

A;Title: The cytoskeletal protein talin is O-glycosylated.

A;Reference number: A42965; MUID:92332560; PMID:1629228

A;Accession: D42965

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HAG>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9

||

Db 1 NI 2

RESULT 37

I54193

Rhesus blood group CcEe protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

C;Accession: I54193

R;Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.;
Colin, Y.

Genomics 19, 68-74, 1994

A;Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe
antigens and characterization of the promoter region.

A;Reference number: I54193; MUID:94245182; PMID:8188244

A;Accession: I54193

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:S70456; NID:g546795; PIDN:AAD14061.1; PID:g4261761

C;Genetics:

A;Gene: GDB:RHCE

A;Cross-references: GDB:229957; OMIM:111700

A;Map position: 1p36.2-1p34

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3

||

Db 3 SK 4

RESULT 38

S57575

T cell receptor V-J junctional alpha chain region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999

C;Accession: S57575

R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argat, V.P.
submitted to the EMBL Data Library, June 1995

A;Description: T cell receptor repertoire for a viral epitope in humans is
diversified by tolerance to a background MHC antigen.

A;Reference number: S57494

A;Accession: S57575

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <BUR>

A;Cross-references: EMBL:Z49953; NID:g887510; PIDN:CAA90224.1; PID:g887511

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2

||

Db 2 AS 3

RESULT 39

S68637

acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 30-Jan-1998

C;Accession: S68637

R;Boschetti, N.; Brodbeck, U.

FEBS Lett. 380, 133-136, 1996

A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of
a single glycosylated protein of 22 kDa.

A;Reference number: S68637; MUID:96181683; PMID:8603722

A;Accession: S68637

A;Molecule type: protein

A;Residues: 1-11 <BOS>

A;Experimental source: brain

C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3

||

Db 7 SK 8

RESULT 40

S78765

ribosomal protein MRP-S24, mitochondrial - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: S78765
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78765
A;Molecule type: protein
A;Residues: 1-11 <GRA>
C;Keywords: mitochondrion
F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
||
Db 6 PK 7

RESULT 41

S54347

tubulin beta chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 07-May-1999

C;Accession: S54347

R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.

Biochem. J. 306, 551-555, 1995

A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glial cells.

A;Reference number: S54343; MUID:95194333; PMID:7887910

A;Accession: S54347

A;Molecule type: protein

A;Residues: 1-11 <OKA>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IK 10
||
Db 10 IK 11

RESULT 42

PN0044

protein kinase C inhibitor I - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998

C;Accession: PN0044

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0044

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 13,900 and the pI is 6.36. The amino-terminus is blocked.
C;Keywords: brain

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KA 11
||
Db 1 KA 2

RESULT 43

PT0217

T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0217

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0217

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 44

C38887

T-cell receptor gamma chain (5a.3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C;Accession: C38887

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.

A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: C38887

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-11 <WHE>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 1 AS 2

RESULT 45

I41946

T-cell receptor gamma chain (5t.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C;Accession: I41946

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.

A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: I41946

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-11 <WHE>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 1 AS 2

RESULT 46

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KK 4
||
Db 5 KK 6

RESULT 47

S65377

cytochrome-c oxidase (EC 1.9.3.1) chain VIa-H, cardiac - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999

C;Accession: S65377

R;Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.

A;Reference number: S65372; MUID:95324529; PMID:7601105

A;Accession: S65377

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.1e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 1 AS 2

RESULT 48

S78422

ribosomal protein RS20, mitochondrial [validated] - rat (tentative sequence) (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78422

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78422

A;Molecule type: protein

A;Residues: 1-11 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein S20

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.1e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KA 11
||
Db 10 KA 11

RESULT 49

PH0939

T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0939

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0939

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2

||

Db 2 AS 3

RESULT 50

PH0940

T-cell receptor beta chain V-D-J region (clone 11) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0940

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0940

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2

||

Db 2 AS 3

RESULT 51

PH0941

T-cell receptor beta chain V-D-J region (clone 12) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0941
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0941
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 52

PH0929

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0929

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0929

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 53

PH0891

T-cell receptor beta chain V-D-J region (clone 6-1) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0891

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0891
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: myelin basic protein-immunized T-cell
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 54

PH0938

T-cell receptor beta chain V-D-J region (clone 9) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0938

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0938

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 55

PH0947

T-cell receptor beta chain V-D-J region (clone A2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0947

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0947

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered from experimentally induced allergic encephalomyelitis

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2

||

Db 2 AS 3

RESULT 56

PH0903

T-cell receptor beta chain V-D-J region (hybridoma S1C2A6) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0903

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0903

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2

||

Db 2 AS 3

RESULT 57

PH0904

T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0904

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0904

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 58

PH0924

T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0924

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0924

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 59

PH0919

T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0919

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0919

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

A;Note: the authors translated the codon CAG for residue 11 as Glu

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 60

PH0914

T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0914

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0914

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 61

PH0922

T-cell receptor beta chain V-D-J region (isolate 8) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0922

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0922

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 62

PH0906

T-cell receptor beta chain V-D-J region (isolates 2, 8, 9) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0906

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0906

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 63

A61575

Trimeresurus serine proteinase (EC 3.4.21.-) - Sakishima habu (fragment)

N;Alternate names: hemorrhagic toxin

C;Species: Trimeresurus elegans (Sakishima habu)

C;Date: 20-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C;Accession: A61575

R;Nikai, T.; Komori, Y.; Imai, K.; Sugihara, H.
Int. J. Biochem. 23, 73-78, 1991

A;Title: Isolation and characterization of hemorrhagic toxin from the venom of Trimeresurus elegans.

A;Reference number: A61575; MUID:91216327; PMID:2022298

A;Accession: A61575

A;Molecule type: protein

A;Residues: 1-11 <NIK>

C;Keywords: hydrolase; serine proteinase; venom

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
||
Db 8 NI 9

RESULT 64

S60294

tubulin 2 beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)

C;Species: Drosophila melanogaster

C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jun-2002

C;Accession: S60294
 R;Chapel, S.; Sobrier, M.L.; Montpied, P.; Micard, D.; Bruhat, A.; Couderc, J.L.; Dastugue, B.
 Insect Mol. Biol. 2, 39-48, 1993
 A;Title: In Drosophila Kc cells 20-OHE induction of the 60C beta-3 tubulin gene expression is a primary transcriptional event.
 A;Reference number: S60292; MUID:97242543; PMID:9087542
 A;Accession: S60294
 A;Molecule type: mRNA
 A;Residues: 1-11 <CHA>
 A;Cross-references: EMBL:X60393
 C;Genetics:
 A;Gene: FlyBase:beta-Tub60D
 A;Cross-references: FlyBase:FBgn0003888

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
 ||
 Db 2 AS 3

RESULT 65

PC2390
 trichorozin I - fungus (Trichoderma harzianum)
 C;Species: Trichoderma harzianum
 C;Date: 17-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Oct-2000
 C;Accession: PC2390
 R;Iida, A.; Sanekata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai, M.; Asami, K.
 Chem. Pharm. Bull. 43, 392-397, 1995
 A;Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichorozins I-IV, from the fungus Trichoderma harzianum.
 A;Reference number: PC2390; MUID:95292356; PMID:7539721
 A;Accession: PC2390
 A;Status: unencoded polypeptide
 A;Molecule type: protein
 A;Residues: 1-11 <IID>
 C;Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers.
 C;Keywords: antibiotic; unencoded polypeptide
 F;1/Modified site: acetylated amino end #status experimental
 F;1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental
 F;11/Modified site: valinol #status experimental

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
 ||
 Db 2 NI 3

RESULT 66

PC2392
 trichorozin III - fungus (*Trichoderma harzianum*)
 C;Species: *Trichoderma harzianum*
 C;Date: 17-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Oct-2000
 C;Accession: PC2392
 R;Iida, A.; Sanekata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai, M.; Asami, K.
 Chem. Pharm. Bull. 43, 392-397, 1995
 A;Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichorozins I-IV, from the fungus *Trichoderma harzianum*.
 A;Reference number: PC2390; MUID:95292356; PMID:7539721
 A;Accession: PC2392
 A;Status: unencoded polypeptide
 A;Molecule type: protein
 A;Residues: 1-11 <IID>
 C;Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers.
 C;Keywords: antibiotic; unencoded polypeptide
 F;1/Modified site: acetylated amino end #status experimental
 F;1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental
 F;11/Modified site: leucinol #status experimental

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
 ||
 Db 2 NI 3

RESULT 67

S52252
 hypothetical protein pco 5'-region - *Escherichia coli* plasmid pRJ1004 (fragment)
 C;Species: *Escherichia coli*
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
 C;Accession: S70166; S52252
 R;Brown, N.L.; Barrett, S.R.; Camakaris, J.; Lee, B.T.O.; Rouch, D.A.
 Mol. Microbiol. 17, 1153-1166, 1995
 A;Title: Molecular genetics and transport analysis of the copper-resistance determinant (pco) from *Escherichia coli* plasmid pRJ1004.
 A;Reference number: S70159; MUID:96130847; PMID:8594334
 A;Accession: S70166
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-11 <BRO>
 A;Cross-references: EMBL:X83541; NID:g619126; PIDN:CAA58524.1; PID:g619127
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 C;Comment: This is the hypothetical translation of a sequence that was not reported as a coding sequence in the complete genome.
 C;Genetics:
 A;Genome: plasmid pRJ1004

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
||
Db 2 NI 3

RESULT 68

I54081

retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999

C;Accession: I54081

R;Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.; Wang, Z.Y.; Larsen, C.J.; Berger, R.

Genes Chromosomes Cancer 6, 133-139, 1993

A;Title: Breakpoint clusters of the PML gene in acute promyelocytic leukemia: primary structure of the reciprocal products of the PML-RARA gene in a patient with t(15;17).

A;Reference number: I54081; MUID:93222087; PMID:7682097

A;Accession: I54081

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <DON>

A;Cross-references: GB:S57794; NID:g299073; PIDN:AAD13888.1; PID:g4261588

A;Note: the translation is from an incorrect reading frame

C;Genetics:

A;Gene: GDB:RARA

A;Cross-references: GDB:120337; OMIM:180240

A;Map position: 17q12-17q12

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
||
Db 10 KR 11

RESULT 69

XAVIBH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994

C;Accession: JC0002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Accession: JC0002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.

C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive;
bradykinin; pyroglutamic acid; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 R 7
|
Db 3 R 3

RESULT 70

ECLQ2M

tachykinin II - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995

C;Accession: S08266

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.

FEBS Lett. 261, 397-401, 1990

A;Title: Locustatachykinin I and II, two novel insect neuropeptides with
homology to peptides of the vertebrate tachykinin family.

A;Reference number: S08265; MUID:90184489; PMID:2311766

A;Accession: S08266

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Superfamily: tachykinin

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 71

GMROL

leucosulfakinin - Madeira cockroach

N;Alternate names: LSK

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996

C;Accession: A01622

R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to
gastrin and cholecystokinin.

A;Reference number: A01622; MUID:86315858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; hormone; sulfoprotein
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 R 7
|
Db 10 R 10

RESULT 72

LFTWWE

probable trpEG leader peptide - *Thermus aquaticus*

C;Species: *Thermus aquaticus*

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C;Accession: S03315

R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.

Biochim. Biophys. Acta 950, 303-312, 1988

A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and trpG.

A;Reference number: S03315; MUID:89000781; PMID:2844259

A;Accession: S03315

A;Molecule type: DNA

A;Residues: 1-11 <SAT>

A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262

A;Note: the source is designated as *Thermus thermophilus* HB8

C;Genetics:

A;Gene: trpL

C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 73

S66196

alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (*Gadus* sp.) (fragment)

C;Species: *Gadus* sp. (cod)

C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998

C;Accession: S66196

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;

Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.

FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and higher vertebrate class I, II, and III forms of the enzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66196

A;Molecule type: protein
A;Residues: 1-11 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 I 9
|
Db 2 I 2

RESULT 74

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003

C;Accession: G42762

R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
Biochemistry 31, 7347-7355, 1992

A;Title: Identification and localization of a cysteinyl residue critical for the
trypsin-like catalytic activity of the proteasome.

A;Reference number: A42762; MUID:92378961; PMID:1510924

A;Accession: G42762

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DIC>

A;Note: sequence extracted from NCBI backbone (NCBIP:112176)

C;Superfamily: multicatalytic endopeptidase complex chain C9

C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 8 K 8

RESULT 75

A33917

dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997

C;Accession: A33917

R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.;
Bergh, S.T.; Evans, D.R.

Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989

A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase
domain and interdomain linker in the CAD multifunctional polypeptide and
properties of the isolated domain.

A;Reference number: A33917; MUID:89282776; PMID:2543974

A;Accession: A33917

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <SIM>

A;Cross-references: GB:M23652

C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase
homology; Bacillus dihydroorotase homology; biotin carboxylase homology;
carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase
(glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase
(glutamine-hydrolyzing) small chain homology; trpG homology

C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3

|

Db 5 K 5

Search completed: April 8, 2004, 15:49:24

Job time : 9.61538 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds
(without alignments)
95.432 Million cell updates/sec

Title: US-09-787-443A-1
Perfect score: 11
Sequence: 1 ASKKPKRNIKA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	11	100.0	11	14	US-10-197-954-28	Sequence 28, Appl
2	4	36.4	11	10	US-09-876-904A-597	Sequence 597, App
3	3	27.3	11	8	US-08-344-824-44	Sequence 44, Appl
4	3	27.3	11	9	US-09-129-112-17	Sequence 17, Appl
5	3	27.3	11	9	US-09-839-666-12	Sequence 12, Appl
6	3	27.3	11	9	US-09-839-884-53	Sequence 53, Appl
7	3	27.3	11	9	US-09-809-739-2	Sequence 2, Appli
8	3	27.3	11	9	US-09-941-611-3	Sequence 3, Appli
9	3	27.3	11	9	US-09-982-264-4	Sequence 4, Appli
10	3	27.3	11	9	US-09-813-333-10	Sequence 10, Appl
11	3	27.3	11	9	US-09-966-871-5	Sequence 5, Appli
12	3	27.3	11	9	US-09-956-522-2	Sequence 2, Appli
13	3	27.3	11	9	US-09-872-832-37	Sequence 37, Appl
14	3	27.3	11	9	US-09-791-378-202	Sequence 202, App
15	3	27.3	11	9	US-09-953-587-31	Sequence 31, Appl
16	3	27.3	11	9	US-09-839-743-16	Sequence 16, Appl
17	3	27.3	11	9	US-09-839-743-17	Sequence 17, Appl
18	3	27.3	11	9	US-09-839-743-18	Sequence 18, Appl
19	3	27.3	11	9	US-09-839-743-24	Sequence 24, Appl
20	3	27.3	11	9	US-09-071-838-39	Sequence 39, Appl
21	3	27.3	11	9	US-09-982-259-4	Sequence 4, Appli
22	3	27.3	11	10	US-09-931-375A-77	Sequence 77, Appl
23	3	27.3	11	10	US-09-906-393A-9	Sequence 9, Appli
24	3	27.3	11	10	US-09-982-265-4	Sequence 4, Appli
25	3	27.3	11	10	US-09-982-287-4	Sequence 4, Appli
26	3	27.3	11	10	US-09-882-291-64	Sequence 64, Appl
27	3	27.3	11	10	US-09-809-391-698	Sequence 698, App
28	3	27.3	11	10	US-09-226-402-31	Sequence 31, Appl
29	3	27.3	11	10	US-09-876-904A-33	Sequence 33, Appl
30	3	27.3	11	10	US-09-876-904A-202	Sequence 202, App
31	3	27.3	11	10	US-09-876-904A-389	Sequence 389, App
32	3	27.3	11	10	US-09-876-904A-591	Sequence 591, App
33	3	27.3	11	10	US-09-876-904A-610	Sequence 610, App
34	3	27.3	11	10	US-09-876-904A-622	Sequence 622, App
35	3	27.3	11	10	US-09-839-884-53	Sequence 53, Appl
36	3	27.3	11	10	US-09-992-665-12	Sequence 12, Appl
37	3	27.3	11	10	US-09-852-910-131	Sequence 131, App
38	3	27.3	11	10	US-09-852-910-248	Sequence 248, App
39	3	27.3	11	10	US-09-865-548A-35	Sequence 35, Appl
40	3	27.3	11	10	US-09-974-992-39	Sequence 39, Appl
41	3	27.3	11	10	US-09-974-992-40	Sequence 40, Appl
42	3	27.3	11	10	US-09-791-524-15	Sequence 15, Appl
43	3	27.3	11	10	US-09-829-922-4	Sequence 4, Appli
44	3	27.3	11	10	US-09-854-248-21	Sequence 21, Appl
45	3	27.3	11	10	US-09-882-171-698	Sequence 698, App
46	3	27.3	11	10	US-09-378-967-4	Sequence 4, Appli
47	3	27.3	11	11	US-09-795-798-13	Sequence 13, Appl
48	3	27.3	11	11	US-09-773-830-10	Sequence 10, Appl
49	3	27.3	11	12	US-10-398-104-197	Sequence 197, App
50	3	27.3	11	12	US-10-458-860-5	Sequence 5, Appli
51	3	27.3	11	12	US-10-344-878-17	Sequence 17, Appl
52	3	27.3	11	12	US-10-371-406B-8	Sequence 8, Appli
53	3	27.3	11	12	US-10-239-103-10	Sequence 10, Appl
54	3	27.3	11	13	US-10-039-645-5	Sequence 5, Appli
55	3	27.3	11	13	US-10-081-281-59	Sequence 59, Appl
56	3	27.3	11	13	US-10-081-281-73	Sequence 73, Appl

57	3	27.3	11	13	US-10-081-281-77	Sequence 77, Appl
58	3	27.3	11	13	US-10-044-703-10	Sequence 10, Appl
59	3	27.3	11	14	US-10-044-995-3	Sequence 3, Appli
60	3	27.3	11	14	US-10-059-261-35	Sequence 35, Appl
61	3	27.3	11	14	US-10-059-261-143	Sequence 143, App
62	3	27.3	11	14	US-10-139-084-5	Sequence 5, Appli
63	3	27.3	11	14	US-10-149-326-12	Sequence 12, Appl
64	3	27.3	11	14	US-10-206-699-238	Sequence 238, App
65	3	27.3	11	14	US-10-211-088-202	Sequence 202, App
66	3	27.3	11	14	US-10-226-007-384	Sequence 384, App
67	3	27.3	11	14	US-10-213-512-39	Sequence 39, Appl
68	3	27.3	11	14	US-10-160-290-4	Sequence 4, Appli
69	3	27.3	11	14	US-10-095-818A-19	Sequence 19, Appl
70	3	27.3	11	14	US-10-234-579-12	Sequence 12, Appl
71	3	27.3	11	14	US-10-079-167-8	Sequence 8, Appli
72	3	27.3	11	14	US-10-224-999A-1343	Sequence 1343, Ap
73	3	27.3	11	14	US-10-224-999A-1344	Sequence 1344, Ap
74	3	27.3	11	14	US-10-224-999A-1345	Sequence 1345, Ap
75	3	27.3	11	14	US-10-224-999A-1346	Sequence 1346, Ap
76	3	27.3	11	14	US-10-224-999A-1347	Sequence 1347, Ap
77	3	27.3	11	14	US-10-239-313A-263	Sequence 263, App
78	3	27.3	11	14	US-10-020-269-7	Sequence 7, Appli
79	3	27.3	11	14	US-10-001-245-216	Sequence 216, App
80	3	27.3	11	14	US-10-387-645-14	Sequence 14, Appl
81	3	27.3	11	14	US-10-161-791-285	Sequence 285, App
82	3	27.3	11	14	US-10-189-437-545	Sequence 545, App
83	3	27.3	11	15	US-10-137-867-486	Sequence 486, App
84	3	27.3	11	15	US-10-016-569A-11	Sequence 11, Appl
85	3	27.3	11	15	US-10-308-644-11	Sequence 11, Appl
86	3	27.3	11	15	US-10-014-099F-30	Sequence 30, Appl
87	3	27.3	11	15	US-10-394-980-98	Sequence 98, Appl
88	3	27.3	11	15	US-10-360-101-187	Sequence 187, App
89	3	27.3	11	15	US-10-408-133-17	Sequence 17, Appl
90	3	27.3	11	15	US-10-411-336A-131	Sequence 131, App
91	3	27.3	11	15	US-10-411-336A-248	Sequence 248, App
92	3	27.3	11	16	US-10-365-761B-2	Sequence 2, Appli
93	2	18.2	11	8	US-08-450-842-45	Sequence 45, Appl
94	2	18.2	11	8	US-08-996-470-2	Sequence 2, Appli
95	2	18.2	11	8	US-08-424-550B-192	Sequence 192, App
96	2	18.2	11	8	US-08-424-550B-550	Sequence 550, App
97	2	18.2	11	8	US-08-809-423A-5	Sequence 5, Appli
98	2	18.2	11	8	US-08-779-457-43	Sequence 43, Appl
99	2	18.2	11	8	US-08-996-140-10	Sequence 10, Appl
100	2	18.2	11	8	US-08-996-140-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-10-197-954-28

; Sequence 28, Application US/10197954

; Publication No. US20030119021A1

; GENERAL INFORMATION:

; APPLICANT: K"ster, Hubert

; APPLICANT: Siddiqi, Suhaib

; APPLICANT: Little, Daniel

```
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-28
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Query Match          100.0%; Score 11; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 ASKKPKRNIKA 11
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Db      1 ASKKPKRNIKA 11
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RESULT 2

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US-09-876-904A-597
; Sequence 597, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 597
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Parechinus angulosus
; FEATURE:
; OTHER INFORMATION: Sea urchin Parechinus angulosus sperm H1 (248 aa).
US-09-876-904A-597
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Query Match          36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKPK 6
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Db 5 KKPK 8

RESULT 3

US-08-344-824-44

; Sequence 44, Application US/08344824

; Publication No. US20030152580A1

; GENERAL INFORMATION:

; APPLICANT: SETTE, Alessandro

; APPLICANT: SIDNEY, John

; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES

; NUMBER OF SEQUENCES: 399

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: One Market Plaza, Steuart Street Tower, 20th

; STREET: Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/344,824

; FILING DATE: 23-NOV-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/278,634

; FILING DATE: 21-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Bastian, Kevin L.

; REGISTRATION NUMBER: 34,774

; REFERENCE/DOCKET NUMBER: 14137-80-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 543-9600

; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-344-824-44

Query Match 27.3%; Score 3; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3

Db |||
 2 ASK 4

RESULT 4

US-09-129-112-17
; Sequence 17, Application US/09129112
; Patent No. US20020019995A1
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume
Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Lotus japonicus
US-09-129-112-17

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
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Db 3 IKA 5

RESULT 5

US-09-839-666-12
; Sequence 12, Application US/09839666
; Patent No. US20020025513A1
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; EXCHANGER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839,666
; FILING DATE: 19-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/737,085
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/0C569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-839-666-12

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Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      6 KRN 8
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Db      5 KRN 7

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RESULT 6
US-09-839-884-53
; Sequence 53, Application US/09839884
; Patent No. US20020076739A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Gelb, Michael H
; APPLICANT: Gygi, Steven
; APPLICANT: Scott, C R
; APPLICANT: Turecek, Frantisek
; APPLICANT: Gerber, Scott A
; APPLICANT: Rist, Beate
; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
; TITLE OF INVENTION: Function in Complex Mixture
; FILE REFERENCE: 64-98A
; CURRENT APPLICATION NUMBER: US/09/839,884
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/383,062
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097,788
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 53
; LENGTH: 11
; TYPE: PRT
; ORGANISM: yeast
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.
US-09-839-884-53

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
|||
Db 4 NIK 6

RESULT 7

US-09-809-739-2

; Sequence 2, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(11)
; OTHER INFORMATION: CDR1 of YFC51.1 light chain
; OTHER INFORMATION: Rat

US-09-809-739-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 2 ASK 4

RESULT 8

US-09-941-611-3

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; Sequence 3, Application US/09941611
; Patent No. US20020106640A1
;   GENERAL INFORMATION:
;       APPLICANT: DELEYS, ROBERT J
;               POLLET, DIRK
;               MAERTENS, GEERT
;               VAN HEUVERSWUN, HUGO
;   TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
;                       ANTIBODIES TO HEPATITIS C VIRUS
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: NIXON & VANDERHYE P.C.
;       STREET: 1100 NORTH GLEBE ROAD
;       CITY: ARLINGTON
;       STATE: VA
;       COUNTRY: USA
;       ZIP: 22201
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/941,611
;       FILING DATE: 30-Aug-2001
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/391,671
;       FILING DATE: 1995-02-21
;       APPLICATION NUMBER: WO PCT/EP91/02409
;       FILING DATE: 13-DEC-1991
;       APPLICATION NUMBER: EP 90124241.2
;       FILING DATE: 14-DEC-1990
;   ATTORNEY/AGENT INFORMATION:
;       NAME: SADOFF, B.J.
;       REGISTRATION NUMBER: 36,663
;       REFERENCE/DOCKET NUMBER: 1487-5
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 7038164000
;       TELEFAX: 7038164100
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 11 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-941-611-3

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Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      6 KRN 8
      |||
Db      5 KRN 7

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RESULT 9

US-09-982-264-4

; Sequence 4, Application US/09982264

; Patent No. US20020106706A1

; GENERAL INFORMATION:

; APPLICANT: Qiu, Bo

; APPLICANT: Stein, Stanley

; APPLICANT: Brunner, Michael

; APPLICANT: Katz, Michael

; APPLICANT: Zhang, Guobao

; APPLICANT: Sigal, Leonard

; TITLE OF INVENTION: Immunological Test Kit with Borellia burgdorferi Epitope

; FILE REFERENCE: 271/288

; CURRENT APPLICATION NUMBER: US/09/982,264

; CURRENT FILING DATE: 2001-10-17

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Borellia burgdorferi

US-09-982-264-4

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5

|||

Db 8 KKP 10

RESULT 10

US-09-813-333-10

; Sequence 10, Application US/09813333

; Patent No. US20020119160A1

; GENERAL INFORMATION:

; APPLICANT: DeGroot, Anne S

; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters

; FILE REFERENCE: 17999-004 US

; CURRENT APPLICATION NUMBER: US/09/813,333

; CURRENT FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: 60/190,834

; PRIOR FILING DATE: 2000-03-20

; NUMBER OF SEQ ID NOS: 81

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

US-09-813-333-10

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
 |||
Db 3 IKA 5

RESULT 11

US-09-966-871-5

; Sequence 5, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; TITLE OF INVENTION: Alterations in Signaling
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-5

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
 |||
Db 5 ASK 7

RESULT 12

US-09-956-522-2

; Sequence 2, Application US/09956522
; Patent No. US20020128203A1
; GENERAL INFORMATION:
; APPLICANT: Schild, Laurent
; APPLICANT: Kellenberger, Stephan
; TITLE OF INVENTION: Methods of Identifying Inhibitory Compounds and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 20349-508
; CURRENT APPLICATION NUMBER: US/09/956,522
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,021
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-956-522-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 3 PKR 5

RESULT 13

US-09-872-832-37

; Sequence 37, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-37

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 2 ASK 4

RESULT 14

US-09-791-378-202

; Sequence 202, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 202
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-202

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
|||
Db 9 NIK 11

RESULT 15

US-09-953-587-31
; Sequence 31, Application US/09953587
; Patent No. US20020142939A1
; GENERAL INFORMATION:
; APPLICANT: CHADA, Kiran K.
; APPLICANT: ASHAR, Hena
; APPLICANT: TKACHENKO, Alex
; APPLICANT: ZHOU, Xianjin
; TITLE OF INVENTION: HMGI PROTEINS IN CANCER AND OBESITY
; FILE REFERENCE: 267/110
; CURRENT APPLICATION NUMBER: US/09/953,587
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 08/852,666
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: US 08/679,529
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: PCT/US/97/21299
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-587-31

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 2 PKR 4

RESULT 16

US-09-839-743-16
; Sequence 16, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:


```
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-16
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          5 PKR 7
            |||
Db          2 PKR 4
```

RESULT 17

US-09-839-743-17

```
; Sequence 17, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
```

; ORGANISM: Nicotiana tabacum
US-09-839-743-17

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 2 PKR 4

RESULT 18

US-09-839-743-18

; Sequence 18, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-18

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 2 PKR 4

RESULT 19

US-09-839-743-24

; Sequence 24, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter

; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-24

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 3 PKR 5

RESULT 20

US-09-071-838-39

; Sequence 39, Application US/09071838
; Patent No. US20020152501A1

; GENERAL INFORMATION:

; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-39

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 NIK 10
      |||
Db      4 NIK 6

```

RESULT 21

US-09-982-259-4

```

; Sequence 4, Application US/09982259
; Publication No. US20020197271A1
; GENERAL INFORMATION:
; APPLICANT: Qiu, Bo
; APPLICANT: Stein, Stanley
; APPLICANT: Brunner, Michael
; APPLICANT: Katz, Michael
; APPLICANT: Zhang, Guobao
; APPLICANT: Sigal, Leonard
; TITLE OF INVENTION: Borellia burgdorferi Epitope Peptides
; FILE REFERENCE: 271/289
; CURRENT APPLICATION NUMBER: US/09/982,259
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Borellia burgdorferi
US-09-982-259-4

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 KKP 5
      |||
Db      8 KKP 10

```

RESULT 22

US-09-931-375A-77

; Sequence 77, Application US/09931375A

; Publication No. US20030027151A1

; GENERAL INFORMATION:

; APPLICANT: WARMAN, Matthew L.

; APPLICANT: GONG, Yaoqin

; APPLICANT: OLSEN, Bjorn R.

; APPLICANT: RAWADI, Georges

; APPLICANT: ROMAN-ROMAN, Sergio

; TITLE OF INVENTION: REGULATOR GENE AND SYSTEM USEFUL FOR THE DIAGNOSIS AND THERAPY OF

; TITLE OF INVENTION: OSTEOPOROSIS

; FILE REFERENCE: 38464-0004

; CURRENT APPLICATION NUMBER: US/09/931,375A

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/304,851

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/234,337

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: US 60/226,119

; PRIOR FILING DATE: 2000-08-18

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 77

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Peptide that can act as an effector of BSMR

US-09-931-375A-77

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KRN 8

|||

Db 4 KRN 6

RESULT 23

US-09-906-393A-9

; Sequence 9, Application US/09906393A

; Publication No. US20030039970A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Zhou

; APPLICANT: Xiao, Wuhan

; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED

; FILE REFERENCE: 1720-1-001CIP

; CURRENT APPLICATION NUMBER: US/09/906,393A

; CURRENT FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 60/218,761

; PRIOR FILING DATE: 2000-07-17

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-9

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 4 KKP 6

RESULT 24

US-09-982-265-4

; Sequence 4, Application US/09982265
; Publication No. US20030040126A1
; GENERAL INFORMATION:
; APPLICANT: Qiu, Bo
; APPLICANT: Stein, Stanley
; APPLICANT: Brunner, Michael
; APPLICANT: Katz, Michael
; APPLICANT: Zhang, Guobao
; APPLICANT: Sigal, Leonard
; TITLE OF INVENTION: Immunological Test Kit with Immunologically Invisible Carrier
; FILE REFERENCE: 271/287
; CURRENT APPLICATION NUMBER: US/09/982,265
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Borellia burgdorferi
US-09-982-265-4

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 8 KKP 10

RESULT 25

US-09-982-287-4

; Sequence 4, Application US/09982287
; Publication No. US20030040127A1
; GENERAL INFORMATION:
; APPLICANT: Qiu, Bo
; APPLICANT: Stein, Stanley
; APPLICANT: Brunner, Michael

; APPLICANT: Katz, Michael
; APPLICANT: Zhang, Guobao
; APPLICANT: Sigal, Leonard
; TITLE OF INVENTION: Multiple Epitopes Connected by Carrier
; FILE REFERENCE: 271/090
; CURRENT APPLICATION NUMBER: US/09/982,287
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Borellia burgdorferi
US-09-982-287-4

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
| | |
Db 8 KKP 10

RESULT 26

US-09-882-291-64
; Sequence 64, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
sequence
US-09-882-291-64

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
| | |
Db 5 SKK 7

RESULT 27

US-09-809-391-698
; Sequence 698, Application US/09809391

; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 698
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-698

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
|||
Db 5 IKA 7

RESULT 28

US-09-226-402-31

; Sequence 31, Application US/09226402
; Publication No. US20030051260A1
; GENERAL INFORMATION:
; APPLICANT: Chada, Kiran K.
; APPLICANT: Ashar, Hena
; APPLICANT: Tkachenko, Alex
; APPLICANT: Zhou, Xianjin
; TITLE OF INVENTION: HMGI Proteins in Cancer and Obesity
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: 758 Springfield Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,402
; FILING DATE: 06 JAN 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD1 037CIPCIP
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 273 4988
; TELEFAX: (908) 273 4679
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-09-226-402-31

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 2 PKR 4

RESULT 29

US-09-876-904A-33
; Sequence 33, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Polyma
virus
; OTHER INFORMATION: major capsid protein VP1
US-09-876-904A-33

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 2 PKR 4

RESULT 30

US-09-876-904A-202

; Sequence 202, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
 THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
 PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 202
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Schizosaccharomyces pombe
 ; FEATURE:
 ; OTHER INFORMATION: Karyophilic peptide
 US-09-876-904A-202

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
 |||
 Db 2 NIK 4

RESULT 31

US-09-876-904A-389

; Sequence 389, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
 THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
 PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 389
 ; LENGTH: 11
 ; TYPE: PRT

; ORGANISM: Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: C. elegans Sdc-3 protein.
US-09-876-904A-389

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 1 SKK 3

RESULT 32

US-09-876-904A-591

; Sequence 591, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 591
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Trout testis H1 (194
aa).
US-09-876-904A-591

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 9 KKP 11

RESULT 33

US-09-876-904A-610

; Sequence 610, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 610
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Bos sp.
 ; FEATURE:
 ; OTHER INFORMATION: Calf Thymus HMG17 (89aa; 9,248 D).
 US-09-876-904A-610

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
 |||
 Db 3 PKR 5

RESULT 34

US-09-876-904A-622

; Sequence 622, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 622
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Trout testis H6 (60 aa).
 US-09-876-904A-622

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 1 KPK 3

RESULT 35

US-09-839-884-53

; Sequence 53, Application US/09839884

; Publication No. US20030087322A9

; GENERAL INFORMATION:

; APPLICANT: Aebersold, Rudolf H.

; APPLICANT: Gelb, Michael H

; APPLICANT: Gygi, Steven

; APPLICANT: Scott, C R

; APPLICANT: Turecek, Frantisek

; APPLICANT: Gerber, Scott A

; APPLICANT: Rist, Beate

; TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein

; TITLE OF INVENTION: Function in Complex Mixture

; FILE REFERENCE: 64-98A

; CURRENT APPLICATION NUMBER: US/09/839,884

; CURRENT FILING DATE: 2001-04-20

; PRIOR APPLICATION NUMBER: 09/383,062

; PRIOR FILING DATE: 1999-08-25

; PRIOR APPLICATION NUMBER: 60/097,788

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 53

; LENGTH: 11

; TYPE: PRT

; ORGANISM: yeast

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (2)

; OTHER INFORMATION: C at position 2 is ICAT-labeled cysteinyl residue.

US-09-839-884-53

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
|||
Db 4 NIK 6

RESULT 36

US-09-992-665-12

; Sequence 12, Application US/09992665

; Publication No. US20030092009A1

; GENERAL INFORMATION:

; APPLICANT: Kaia Palm

; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE

; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-12

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 4 KPK 6

RESULT 37

US-09-852-910-131

; Sequence 131, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor Signaling

; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 131
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: G alpha t library peptide
US-09-852-910-131

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
|||
Db 4 NIK 6

RESULT 38

US-09-852-910-248

; Sequence 248, Application US/09852910
 ; Publication No. US20030096297A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hamm, Heidi
 ; APPLICANT: Gilchrist, Annette
 ; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor Signaling
 ; FILE REFERENCE: 2661-101
 ; CURRENT APPLICATION NUMBER: US/09/852,910
 ; CURRENT FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: US 60/275,472
 ; PRIOR FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 271
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 248
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(11)
 ; OTHER INFORMATION: G11 library peptide
 US-09-852-910-248

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
 |||
 Db 4 KPK 6

RESULT 39

US-09-865-548A-35

; Sequence 35, Application US/09865548A
 ; Publication No. US20030096298A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barnea, Eilon
 ; APPLICANT: Beer, Ilan
 ; APPLICANT: Ziv, Tamar
 ; APPLICANT: Admon, Arie
 ; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES,
 ; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
 ; FILE REFERENCE: 01/22080
 ; CURRENT APPLICATION NUMBER: US/09/865,548A
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: US 60/290,958
 ; PRIOR FILING DATE: 2001-05-16
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 35

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-35

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 2 ASK 4

RESULT 40

US-09-974-992-39

; Sequence 39, Application US/09974992
; Publication No. US20030138866A1
; GENERAL INFORMATION:
; APPLICANT: Mathiesen, Marianne J.
; APPLICANT: Theisen, Michael
; APPLICANT: Holm, Arne
; APPLICANT: Ostergaard, Soren
; TITLE OF INVENTION: No. US20030138866A1el OspC-derived peptide fragments
; FILE REFERENCE: 459-666P
; CURRENT APPLICATION NUMBER: US/09/974,992
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/180,089
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: PCT/DK97/00203
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Substitution
; OTHER INFORMATION: analogue of OspC peptide
US-09-974-992-39

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 9 KKP 11

RESULT 41

US-09-974-992-40

; Sequence 40, Application US/09974992
; Publication No. US20030138866A1


```

; GENERAL INFORMATION:
; APPLICANT: Mathiesen, Marianne J.
; APPLICANT: Theisen, Michael
; APPLICANT: Holm, Arne
; APPLICANT: Ostergaard, Soren
; TITLE OF INVENTION: No. US20030138866A1el OspC-derived peptide fragments
; FILE REFERENCE: 459-666P
; CURRENT APPLICATION NUMBER: US/09/974,992
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/180,089
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: PCT/DK97/00203
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Substitution
; OTHER INFORMATION: analogue of OspC c-terminal peptide
; OTHER INFORMATION: Xaa is 6-aminohexanoic acid
US-09-974-992-40

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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Qy      3 KKP 5
        |||
Db      9 KKP 11

```

RESULT 42

```

US-09-791-524-15
; Sequence 15, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of
Heterologous Genes
; FILE REFERENCE: A3319A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524-15

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```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 2 SKK 4

RESULT 43

US-09-829-922-4

; Sequence 4, Application US/09829922
; Publication No. US20030171537A1
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
; APPLICANT: Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; TITLE OF INVENTION: function
; FILE REFERENCE: 2973.19998
; CURRENT APPLICATION NUMBER: US/09/829,922
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 08/894,327
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: pctus96/01535
; PRIOR FILING DATE: 1996-02-16
; PRIOR APPLICATION NUMBER: 08/392,542
; PRIOR FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-922-4

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
|||
Db 9 SKK 11

RESULT 44

US-09-854-248-21

; Sequence 21, Application US/09854248
; Publication No. US20030175247A1
; GENERAL INFORMATION:
; APPLICANT: Salgaller, Michael L.
; APPLICANT: Boynton, Alton L.
; TITLE OF INVENTION: METHOD TO INCREASE CLASS I PRESENTATION OF EXOGENOUS
; TITLE OF INVENTION: ANTIGENS BY HUMAN DENDRITIC CELLS
; FILE REFERENCE: 20093-8-1US
; CURRENT APPLICATION NUMBER: US/09/854,248
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/203,758
; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-248-21

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
|||
Db 7 NIK 9

RESULT 45

US-09-882-171-698

; Sequence 698, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,313
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,672
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315

; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,893
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,630
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,878
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,662
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,872
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,882
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,637
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,903
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,888
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,879
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23

```

; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

```

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Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 IKA 11
        |||
Db      5 IKA 7

```

RESULT 46

US-09-378-967-4

```
; Sequence 4, Application US/09378967
; Publication No. US20030185818A1
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN J.
; APPLICANT: CROWE, J. SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,967
; FILING DATE: 23-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,313
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,067
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01289
; FILING DATE: 15-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9115364.3
; FILING DATE: 16-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WENDLER, HELEN E.
; REGISTRATION NUMBER: 37,964
; REFERENCE/DOCKET NUMBER: LYNX91-01A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-378-967-4
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Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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QY 1 ASK 3
|||
Db 2 ASK 4

RESULT 47

US-09-795-798-13

; Sequence 13, Application US/09795798

; Publication No. US20030207336A1

; GENERAL INFORMATION:

; APPLICANT: Presta, Leonard G.

; Jardieu, Paula M.

; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/795,798

; FILING DATE: 28-Feb-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/974,899

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P1014R1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1994

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-795-798-13

Query Match 27.3%; Score 3; DB 11; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
|||
Db 2 ASK 4

RESULT 48

US-09-773-830-10

```
; Sequence 10, Application US/09773830
; Publication No. US20030220482A1
; GENERAL INFORMATION:
; APPLICANT: Ziwei Huang
; APPLICANT: Jiansong Luo
; APPLICANT: Zhaowen Luo
; APPLICANT: Naming Zhou
; TITLE OF INVENTION: A No. US20030220482A1e1 Peptide Antagonist of CXCR4
; TITLE OF INVENTION: Derived from the N-Terminus of Viral Chemokine vMIP-II
; FILE REFERENCE: HUA01-NP007
; CURRENT APPLICATION NUMBER: US/09/773,830
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/180,487
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: v-MIPII derived peptide
US-09-773-830-10
```

```
Query Match          27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 ASK 3
      |||
Db      6 ASK 8
```

RESULT 49

US-10-398-104-197

```
; Sequence 197, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 197
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-197

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKR 7
|||
Db 7 PKR 9

RESULT 50

US-10-458-860-5
; Sequence 5, Application US/10458860
; Publication No. US20040049800A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Rapid Methods For Assessing Therapeutic
; TITLE OF INVENTION: Activity Using Animals Expressing Constitutively Active
G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: 00398/517002
; CURRENT APPLICATION NUMBER: US/10/458,860
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/388,450
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic fragment
US-10-458-860-5

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 5 ASK 7

RESULT 51

US-10-344-878-17
; Sequence 17, Application US/10344878
; Publication No. US20040053848A1
; GENERAL INFORMATION:

```

; APPLICANT: The University of Virginia Patent Foundation
; APPLICANT: Allis, C. David
; APPLICANT: Strahl, Brian D
; TITLE OF INVENTION: Antibodies Specific for Methylated Lysines in Histones
; FILE REFERENCE: 00601-02
; CURRENT APPLICATION NUMBER: US/10/344,878
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/227,767
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/302,747
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide used to raise antibodies against the H3
amino
; OTHER INFORMATION: terminus having MeLys at the fifth amino acid position
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: METHYLATION
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)..(11)
; OTHER INFORMATION: artificial amino acids added to the natural histone
sequence to
; OTHER INFORMATION: aid in the production of the antibody
US-10-344-878-17

```

```

Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 KKP 5
      |||
Db      5 KKP 7

```

```

RESULT 52
US-10-371-406B-8
; Sequence 8, Application US/10371406B
; Publication No. US20040053828A1
; GENERAL INFORMATION:
; APPLICANT: Mayo, Kevin H.
; APPLICANT: Hoyer, Thomas R.
; APPLICANT: Flader Lavey, Carolee
; TITLE OF INVENTION: Partial Peptide Mimetics and Methods
; FILE REFERENCE: 110.01710101
; CURRENT APPLICATION NUMBER: US/10/371,406B
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/359,272
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 17

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-371-406B-8

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIK 10
|||
Db 2 NIK 4

RESULT 53

US-10-239-103-10
; Sequence 10, Application US/10239103
; Publication No. US20040057961A1
; GENERAL INFORMATION:
; APPLICANT: Brown University Research Foundation
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004-061
; CURRENT APPLICATION NUMBER: US/10/239,103
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 09/813,333
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-10

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
|||
Db 3 IKA 5

RESULT 54

US-10-039-645-5
; Sequence 5, Application US/10039645
; Publication No. US20020147170A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin

; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; TITLE OF INVENTION: and No. US20020147170A1functional Receptors as No.
US20020147170A1 Therapeutic Agents
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-5

Query Match 27.3%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 5 ASK 7

RESULT 55

US-10-081-281-59
; Sequence 59, Application US/10081281
; Publication No. US20020151707A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; Gross, Jane A.
; Sheppard, Paul
; TITLE OF INVENTION: Immune Mediators and Related Methods
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,281
; FILING DATE: 20-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/261,811A
; FILING DATE: 03-Mar-1999
; APPLICATION NUMBER: US 08/480,002
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/482,133

```

;          FILING DATE: 07-JUN-1995
;          APPLICATION NUMBER: US 08/483,241
;          FILING DATE: 07-JUN-1995
;          APPLICATION NUMBER: US 60/005,964
;          FILING DATE: 27-OCT-1995
;          APPLICATION NUMBER: US 08/657,581
;          FILING DATE: 07-JUN-1996
;          ATTORNEY/AGENT INFORMATION:
;          NAME: Parent, Annette S.
;          REGISTRATION NUMBER: 42,058
;          REFERENCE/DOCKET NUMBER: 014058-005630US
;          TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (415) 576-0200
;          TELEFAX: (415) 576-0300
;          INFORMATION FOR SEQ ID NO: 59:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 11 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: <Unknown>
;          TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          FEATURE:
;          NAME/KEY: Modified-site
;          LOCATION: 11
;          OTHER INFORMATION: /product= "OTHER"
;          /note= "Xaa = threoninamide"
;          SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-081-281-59

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Query Match          27.3%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 IKA 11
            |||
Db          1 IKA 3

```

RESULT 56

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US-10-081-281-73
; Sequence 73, Application US/10081281
; Publication No. US20020151707A1
;   GENERAL INFORMATION:
;   APPLICANT: Kindsvogel, Wayne
;               Gross, Jane A.
;               Sheppard, Paul
;   TITLE OF INVENTION: Immune Mediators and Related Methods
;   NUMBER OF SEQUENCES: 121
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk

```

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;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/081,281
;      FILING DATE: 20-Feb-2002
;      CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/09/261,811A
;      FILING DATE: 03-Mar-1999
;      APPLICATION NUMBER: US 08/480,002
;      FILING DATE: 07-JUN-1995
;      APPLICATION NUMBER: US 08/482,133
;      FILING DATE: 07-JUN-1995
;      APPLICATION NUMBER: US 08/483,241
;      FILING DATE: 07-JUN-1995
;      APPLICATION NUMBER: US 60/005,964
;      FILING DATE: 27-OCT-1995
;      APPLICATION NUMBER: US 08/657,581
;      FILING DATE: 07-JUN-1996
;
; ATTORNEY/AGENT INFORMATION:
;      NAME: Parent, Annette S.
;      REGISTRATION NUMBER: 42,058
;      REFERENCE/DOCKET NUMBER: 014058-005630US
;
; TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 576-0200
;      TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 73:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 11 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: <Unknown>
;          TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      FEATURE:
;          NAME/KEY: Modified-site
;          LOCATION: 11
;          OTHER INFORMATION: /product= "OTHER"
;          /note= "Xaa = glutamic acid amide"
;      SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-10-081-281-73

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Query Match          27.3%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 IKA 11
        |||
Db      5 IKA 7

```

```

RESULT 57
US-10-081-281-77
; Sequence 77, Application US/10081281
; Publication No. US20020151707A1
; GENERAL INFORMATION:
;      APPLICANT: Kindsvogel, Wayne

```

```

;           Gross, Jane A.
;           Sheppard, Paul
;   TITLE OF INVENTION: Immune Mediators and Related Methods
;   NUMBER OF SEQUENCES: 121
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Townsend and Townsend and Crew LLP
;       STREET: Two Embarcadero Center, Eighth Floor
;       CITY: San Francisco
;       STATE: California
;       COUNTRY: USA
;       ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/081,281
;       FILING DATE: 20-Feb-2002
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/09/261,811A
;       FILING DATE: 03-Mar-1999
;       APPLICATION NUMBER: US 08/480,002
;       FILING DATE: 07-JUN-1995
;       APPLICATION NUMBER: US 08/482,133
;       FILING DATE: 07-JUN-1995
;       APPLICATION NUMBER: US 08/483,241
;       FILING DATE: 07-JUN-1995
;       APPLICATION NUMBER: US 60/005,964
;       FILING DATE: 27-OCT-1995
;       APPLICATION NUMBER: US 08/657,581
;       FILING DATE: 07-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Parent, Annette S.
;       REGISTRATION NUMBER: 42,058
;       REFERENCE/DOCKET NUMBER: 014058-005630US
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (415) 576-0200
;       TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 77:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 11 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       FEATURE:
;           NAME/KEY: Modified-site
;           LOCATION: 11
;           OTHER INFORMATION: /product= "OTHER"
;                               /note= "Xaa = methioninamide"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-081-281-77

```

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Query Match          27.3%;  Score 3;  DB 13;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 8.3e+03;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
|||
Db 7 IKA 9

RESULT 58

US-10-044-703-10

; Sequence 10, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-10

Query Match 27.3%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
|||
Db 3 IKA 5

RESULT 59

US-10-044-995-3

; Sequence 3, Application US/10044995
; Publication No. US20030049685A1
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; POLLET, DIRK
; MAERTENS, GEERT
; VAN HEUVERSUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/044,995
;      FILING DATE: 15-Jan-2002
;      CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/391,671
;      FILING DATE: <Unknown>
;      APPLICATION NUMBER: US 07/920,286
;      FILING DATE: 14-OCT-1992
;      APPLICATION NUMBER: WO PCT/EP91/02409
;      FILING DATE: 13-DEC-1991
;      APPLICATION NUMBER: EP 90124241.2
;      FILING DATE: 14-DEC-1990
;
; ATTORNEY/AGENT INFORMATION:
;      NAME: SADOFF, B.J.
;      REGISTRATION NUMBER: 36,663
;      REFERENCE/DOCKET NUMBER: 1487-5
;
; TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 7038164000
;      TELEFAX: 7038164100
;
; INFORMATION FOR SEQ ID NO: 3:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 11 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-044-995-3

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 KRN 8
      |||
Db      5 KRN 7

```

```

RESULT 60
US-10-059-261-35
; Sequence 35, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29

```

; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-
ScFv461
; OTHER INFORMATION: peptide sequence
US-10-059-261-35

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 4 KPK 6

RESULT 61

US-10-059-261-143

; Sequence 143, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-
ScFv350
; OTHER INFORMATION: peptide sequence
US-10-059-261-143

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6

Db |||
 4 KPK 6

RESULT 62

US-10-139-084-5

; Sequence 5, Application US/10139084
; Publication No. US20030087313A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Dose Response-Based Methods For
; TITLE OF INVENTION: Identifying Receptors Having Alterations in Signaling
; FILE REFERENCE: 00398/515002
; CURRENT APPLICATION NUMBER: US/10/139,084
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/288,647
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-084-5

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
 |||
Db 5 ASK 7

RESULT 63

US-10-149-326-12

; Sequence 12, Application US/10149326
; Publication No. US20030100492A1
; GENERAL INFORMATION:
; APPLICANT: Yayon, Avner
; TITLE OF INVENTION: PROTEOGLYCANS AND PHARMACEUTICAL COMPOSITIONS COMPRISING
THEM
; FILE REFERENCE: 01/22063
; CURRENT APPLICATION NUMBER: US/10/149,326
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: IL 133318
; PRIOR FILING DATE: 1999-12-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-149-326-12

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 6 KKP 8

RESULT 64

US-10-206-699-238
; Sequence 238, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain
Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-238

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
|||
Db 8 KKP 10

RESULT 65

US-10-211-088-202
; Sequence 202, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For
Molecular Binding

```

; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
US-10-211-088-202

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 PKR 7
      |||
Db      2 PKR 4

```

RESULT 66

```

US-10-226-007-384
; Sequence 384, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 384
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vesicular stomatitis virus
US-10-226-007-384

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SKK 4
      |||
Db      1 SKK 3

```

RESULT 67

US-10-213-512-39

```
; Sequence 39, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-39
```

```
Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      8 NIK 10
      |||
Db      4 NIK 6
```

RESULT 68

US-10-160-290-4

```
; Sequence 4, Application US/10160290
; Publication No. US20030124557A1
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
;           Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides nad Peptidomimetics with
;                   Structural Similarity to Human p53 That Activate
;                   p53
;                   Function
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
```

```

; COUNTRY: U.S.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/160,290
; FILING DATE: 04-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/685,027
; FILING DATE: 10-Oct-2000
; APPLICATION NUMBER: 08/392,542
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 0486.48439
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9100
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-160-290-4

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```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SKK 4
      |||
Db      9 SKK 11

```

```

RESULT 69
US-10-095-818A-19
; Sequence 19, Application US/10095818A
; Publication No. US20030124613A1
; GENERAL INFORMATION:
; APPLICANT: Hildebrand, William H
; APPLICANT: Buchli, Rico
; APPLICANT: Prilliman, Kiley R
; APPLICANT: Hickman, Heather D
; TITLE OF INVENTION: EPITOPE TESTING USING SOLUBLE HLA
; FILE REFERENCE: 6680.042
; CURRENT APPLICATION NUMBER: US/10/095,818A
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/274,605
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/362,799

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; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 10/022,066
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-095-818A-19

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASK 3
|||
Db 2 ASK 4

RESULT 70

US-10-234-579-12

; Sequence 12, Application US/10234579
; Publication No. US20030129587A1
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; EXCHANGER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,579
; FILING DATE: 30-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,085
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/0C569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237

```

;           TELEX: 236687
;   INFORMATION FOR SEQ ID NO: 12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-234-579-12

```

```

Query Match          27.3%;  Score 3;  DB 14;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 8.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      6 KRN 8
        |||
Db      5 KRN 7

```

RESULT 71

US-10-079-167-8

```

; Sequence 8, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-079-167-8

```

```

Query Match          27.3%;  Score 3;  DB 14;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 8.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

Qy 1 ASK 3
|||
Db 1 ASK 3

RESULT 72

US-10-224-999A-1343
; Sequence 1343, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1343
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1343

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 9 KPK 11

RESULT 73

US-10-224-999A-1344
; Sequence 1344, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1344
; LENGTH: 11

; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1344

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 8 KPK 10

RESULT 74

US-10-224-999A-1345
; Sequence 1345, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1345
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1345

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 7 KPK 9

RESULT 75

US-10-224-999A-1346
; Sequence 1346, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A

; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1346
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1346

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KPK 6
|||
Db 6 KPK 8

Search completed: April 8, 2004, 16:35:32
Job time : 32.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds
(without alignments)
124.984 Million cell updates/sec

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Title:      US-09-787-443A-1
Perfect score:  11
Sequence:    1 ASKKPKRNIKA 11
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

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Minimum DB seq length: 11
Maximum DB seq length: 11
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Post-processing: Listing first 100 summaries

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Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score	Match	Length	DB	ID	Description

1	3	27.3	11	2	Q9S618	Q9s618 prochloroco
2	3	27.3	11	5	Q25916	Q25916 plasmodium
3	3	27.3	11	5	Q95PX6	Q95px6 caenorhabdi
4	3	27.3	11	6	Q9TQS0	Q9tqs0 bos taurus
5	3	27.3	11	9	Q38415	Q38415 bacterioph
6	3	27.3	11	10	Q04131	Q04131 lycopersico
7	3	27.3	11	12	Q86866	Q86866 lymphocytic
8	3	27.3	11	12	Q86864	Q86864 lymphocytic
9	3	27.3	11	12	Q86868	Q86868 lymphocytic
10	2	18.2	11	2	Q9R790	Q9r790 borrelia ga
11	2	18.2	11	2	Q47451	Q47451 escherichia
12	2	18.2	11	2	Q9AI27	Q9aiz7 carsonella
13	2	18.2	11	2	Q8RKN1	Q8rkn1 escherichia
14	2	18.2	11	2	Q9L4F7	Q9l4f7 bacillus ce
15	2	18.2	11	2	P77404	P77404 escherichia
16	2	18.2	11	2	Q9RQ60	Q9rq60 buchnera ap
17	2	18.2	11	2	P71228	P71228 escherichia
18	2	18.2	11	2	Q93MI7	Q93mi7 escherichia
19	2	18.2	11	2	Q9RFZ2	Q9rfz2 mycoplasma
20	2	18.2	11	2	P95518	P95518 pasteurella
21	2	18.2	11	2	Q47345	Q47345 escherichia
22	2	18.2	11	2	Q9AI28	Q9aiz8 carsonella
23	2	18.2	11	2	Q44090	Q44090 acholeplasm
24	2	18.2	11	2	Q44237	Q44237 anabaena sp
25	2	18.2	11	2	Q9R872	Q9r872 escherichia
26	2	18.2	11	2	Q9R446	Q9r446 neisseria g
27	2	18.2	11	2	Q8GMU3	Q8gmu3 acinetobact
28	2	18.2	11	2	Q8GL24	Q8gl24 borrelia bu
29	2	18.2	11	2	Q8GL19	Q8gl19 borrelia bu
30	2	18.2	11	2	Q7X566	Q7x566 thermus the
31	2	18.2	11	4	O60761	O60761 homo sapien
32	2	18.2	11	4	O75811	O75811 homo sapien
33	2	18.2	11	4	Q9H4H5	Q9h4h5 homo sapien
34	2	18.2	11	4	Q15997	Q15997 homo sapien
35	2	18.2	11	4	Q9UCP5	Q9ucp5 homo sapien
36	2	18.2	11	4	Q9UBM2	Q9ubm2 homo sapien
37	2	18.2	11	4	Q9H3V7	Q9h3v7 homo sapien
38	2	18.2	11	4	Q8NI03	Q8ni03 homo sapien
39	2	18.2	11	5	Q26092	Q26092 pisaster oc
40	2	18.2	11	5	Q9NL65	Q9nl65 ascaris suu
41	2	18.2	11	5	Q9TWX6	Q9twx6 manduca sex
42	2	18.2	11	5	Q8MPQ3	Q8mpq3 caenorhabdi
43	2	18.2	11	5	Q86D32	Q86d32 trypanosoma
44	2	18.2	11	5	Q86D31	Q86d31 trypanosoma
45	2	18.2	11	6	Q9TRR7	Q9trr7 oryctolagus
46	2	18.2	11	6	Q9TTQ0	Q9ttq0 gorilla gor
47	2	18.2	11	7	O77872	O77872 oreochromis
48	2	18.2	11	7	O77880	O77880 oreochromis
49	2	18.2	11	7	O77908	O77908 oreochromis
50	2	18.2	11	7	O77873	O77873 oreochromis
51	2	18.2	11	7	O77871	O77871 oreochromis
52	2	18.2	11	7	O77907	O77907 oreochromis
53	2	18.2	11	7	O77897	O77897 oreochromis
54	2	18.2	11	7	Q7YP62	Q7yp62 homo sapien
55	2	18.2	11	8	Q8ME62	Q8me62 porphyra ca
56	2	18.2	11	8	Q8MEL7	Q8mel7 sida hooker
57	2	18.2	11	8	Q9G5Y0	Q9g5y0 pseudotrape

58	2	18.2	11	8	Q8MEM2	Q8mem2 lagunaria p
59	2	18.2	11	8	Q8MES5	Q8mes5 abelmoschus
60	2	18.2	11	8	Q8MEP0	Q8mep0 hibiscus pe
61	2	18.2	11	8	Q8MER8	Q8mer8 dombeya til
62	2	18.2	11	8	Q32704	Q32704 nicotiana t
63	2	18.2	11	8	Q8MES1	Q8mes1 alyogyne pi
64	2	18.2	11	8	Q8MEP3	Q8mep3 hibiscus no
65	2	18.2	11	8	Q8MEQ7	Q8meq7 hibiscus dr
66	2	18.2	11	8	Q8MEL9	Q8mel9 pavonia has
67	2	18.2	11	8	Q8MER0	Q8mer0 hibiscus co
68	2	18.2	11	8	Q8MES3	Q8mes3 alyogyne cr
69	2	18.2	11	8	Q8MEP5	Q8mep5 hibiscus mi
70	2	18.2	11	8	Q8MER1	Q8mer1 hibiscus ca
71	2	18.2	11	8	Q8SKP8	Q8skp8 ctenophorus
72	2	18.2	11	8	Q8MER7	Q8mer7 fioria viti
73	2	18.2	11	8	Q8HQX5	Q8hqx5 rhabdothamn
74	2	18.2	11	8	Q7Y9H0	Q7y9h0 hypsilurus
75	2	18.2	11	9	Q37925	Q37925 bacteriopha
76	2	18.2	11	10	Q06626	Q06626 solanum tub
77	2	18.2	11	10	O65901	O65901 leavenworth
78	2	18.2	11	10	Q8RV30	Q8rv30 zea mays (m
79	2	18.2	11	10	Q8RUE7	Q8rue7 zea mays (m
80	2	18.2	11	10	P82436	P82436 nicotiana t
81	2	18.2	11	10	P82336	P82336 pisum sativ
82	2	18.2	11	10	Q7X9Y3	Q7x9y3 cucumis sat
83	2	18.2	11	11	Q9QXM6	Q9qxm6 mus musculu
84	2	18.2	11	11	Q99N81	Q99n81 mus musculu
85	2	18.2	11	11	Q9JLE6	Q9jle6 rattus norv
86	2	18.2	11	11	Q8R2J7	Q8r2j7 mesocricetu
87	2	18.2	11	11	Q9QXN6	Q9qxn6 mus musculu
88	2	18.2	11	11	Q7TME3	Q7tme3 mus musculu
89	2	18.2	11	12	P89269	P89269 xestia c-ni
90	2	18.2	11	12	Q997C1	Q997c1 east africa
91	2	18.2	11	12	Q86565	Q86565 varicella-z
92	2	18.2	11	12	Q80GN9	Q80gn9 tomato leaf
93	2	18.2	11	12	Q69269	Q69269 equine herp
94	2	18.2	11	13	Q8AX69	Q8ax69 oreochromis
95	2	18.2	11	13	Q8AX68	Q8ax68 oreochromis
96	2	18.2	11	13	Q7ZZI9	Q7zzi9 motacilla f
97	2	18.2	11	13	Q7ZZI6	Q7zzi6 motacilla f
98	2	18.2	11	15	Q85620	Q85620 moloney mur
99	1	9.1	11	2	Q9AIY6	Q9aiy6 carsonella
100	1	9.1	11	2	O68237	O68237 borrelia bu

ALIGNMENTS

RESULT 1

Q9S618

ID Q9S618 PRELIMINARY; PRT; 11 AA.

AC Q9S618;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE Cytochrome b6/f complex subunit IV (Fragment).

GN PETD.

OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 sorted from the Sargasso Sea and Gulf Stream."
 RL Limnol. Oceanog. 43:1615-1630(1998).
 DR EMBL; AF070132; AAD20740.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
 |||
 Db 5 KKP 7

RESULT 2

Q25916

ID Q25916 PRELIMINARY; PRT; 11 AA.
 AC Q25916;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Malaria antigen (7H8/2) (Fragment).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91164876; PubMed=1706114;
 RA Limpiaiboon T., Taylor D., Jones G., Geysen H.M., Saul A.;
 RT "Characterization of a Plasmodium falciparum epitope recognized by a
 monoclonal antibody with broad isolate and species specificity."
 RL Southeast Asian J. Trop. Med. Public Health 21:388-396(1990).
 DR EMBL; M31305; AAA29645.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1415 MW; DB03D3BC42C33699 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RNI 9
 |||
 Db 9 RNI 11

RESULT 3

Q95PX6

ID Q95PX6 PRELIMINARY; PRT; 11 AA.

AC Q95PX6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN ZK1236.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Favello A.;
 RT "The sequence of C. elegans cosmid ZK1236.";
 RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; L13200; AAL11108.1; -.
 DR WormPep; ZK1236.8; CE29629.
 KW Hypothetical protein.
 SQ SEQUENCE 11 AA; 1304 MW; DFA3510A25A76322 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
 |||
 Db 7 SKK 9

RESULT 4

Q9TQS0

ID Q9TQS0 PRELIMINARY; PRT; 11 AA.
 AC Q9TQS0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE C-KIT (Fragment).
 GN KIT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
 RT "A polymorphism in the bovine c-kit gene."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ243424; CAB60775.1; -.
 DR EMBL; AJ243060; CAB60774.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 27.3%; Score 3; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
 |||
 Db 1 IKA 3

RESULT 5

Q38415

ID Q38415 PRELIMINARY; PRT; 11 AA.
 AC Q38415;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ant1 protein (Fragment).
 OS Bacteriophage P7.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC P1-like viruses.
 OX NCBI_TaxID=10682;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90335968; PubMed=1696181;
 RA Citron M., Schuster H.;
 RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs."
 RL Cell 62:591-598(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92319637; PubMed=1620606;
 RA Citron M., Schuster H.;
 RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense
 RT RNA."
 RL Nucleic Acids Res. 20:3085-3090(1992).
 DR EMBL; M35139; AAA32437.1; -.
 DR PIR; S42449; S42449.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1315 MW; 38A55C6D11B2C737 CRC64;

Query Match 27.3%; Score 3; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKP 5
 |||

Db 2 KKP 4

RESULT 6

Q04131

ID Q04131 PRELIMINARY; PRT; 11 AA.
AC Q04131;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wound induced protein (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=pik-red; TISSUE=Pericarp;
RX MEDLINE=91355936; PubMed=1715787;
RA Parsons B.L., Mattoo A.K.;
RT "Wound regulated accumulation of specific transcripts in tomato fruit:
RT interactions with fruit development, ethylene and light.";
RL Plant Mol. Biol. 17:453-464(1991).
DR EMBL; X59884; CAA42539.1; -.
DR PIR; S19775; S19775.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKK 4
| | |
Db 4 SKK 6

RESULT 7

Q86866

ID Q86866 PRELIMINARY; PRT; 11 AA.
AC Q86866;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE S-RNA product protein (Fragment).
GN S-RNA PRODUCT.
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=11623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopid D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).

DR EMBL; S75748; AAB33668.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1200 MW; 54235C80D9C45B57 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
|||
Db 1 IKA 3

RESULT 8

Q86864

ID Q86864 PRELIMINARY; PRT; 11 AA.
AC Q86864;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LCMV viral protein (Fragment).
GN LCMV VIRAL PROTEIN.
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=11623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskophidis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus."
RL J. Virol. 69:2187-2193(1995).
DR EMBL; S75739; AAB33665.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1186 MW; D6235C80D9C45B42 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
|||
Db 1 IKA 3

RESULT 9

Q86868

ID Q86868 PRELIMINARY; PRT; 11 AA.
AC Q86868;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE S-RNA product protein (Fragment).
GN S-RNA PRODUCT.
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=11623;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95190990; PubMed=7533851;
 RA Moskophidis D., Zinkernagel R.M.;
 RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
 RT choriomeningitis virus.";
 RL J. Virol. 69:2187-2193(1995).
 DR EMBL; S75751; AAB33671.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1200 MW; 54235C80D9C45B57 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IKA 11
 |||
 Db 1 IKA 3

RESULT 10

Q9R790

ID Q9R790 PRELIMINARY; PRT; 11 AA.
 AC Q9R790;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Outer surface protein C (Fragment).
 GN OSPC.
 OS Borrelia garinii.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=29519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G25;
 RX MEDLINE=97426044; PubMed=9282748;
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "he Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene.";
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL; U93700; AAC45535.1; -.
 DR GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR001800; Lipoprotein_6.
 DR Pfam; PF01441; Lipoprotein_6; 1.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KK 4
 ||
 Db 2 KK 3

RESULT 11

Q47451

ID Q47451 PRELIMINARY; PRT; 11 AA.
 AC Q47451;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Plasmid pRJ1004 DNA (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=pRJ1004;
 RX MEDLINE=96130847; PubMed=8594334;
 RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T., Rouch D.A.;
 RT "Molecular genetics and transport analysis of the copper-resistance
 RT determinants (pco) from Escherichia coli plasmid pRJ1004."
 RL Mol. Microbiol. 17:1153-1166(1995).
 DR EMBL; X83541; CAA58524.1; -.
 DR PIR; S70166; S52252.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1195 MW; 47D864F8ADC1A057 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
 ||
 Db 2 NI 3

RESULT 12

Q9AIZ7

ID Q9AIZ7 PRELIMINARY; PRT; 11 AA.
 AC Q9AIZ7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Tryptophanyl-tRNA synthetase (Fragment).
 GN TRPS.
 OS Carsonella ruddii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
 OX NCBI_TaxID=114186;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20336438; PubMed=10877784;
 RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
 RA Baumann P.;
 RT "Cospeciation of psyllids and their primary prokaryotic
 RT endosymbionts."
 RL Appl. Environ. Microbiol. 66:2898-2905(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21125546; PubMed=11222582;
 RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
 RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
 RL J. Bacteriol. 183:1853-1861(2001).
 DR EMBL; AF211132; AAK15377.1; -.
 DR GO; GO:0004812; F:tRNA ligase activity; IEA.
 KW Aminoacyl-tRNA synthetase.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1333 MW; A28C67D6533059C6 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IK 10
 ||
 Db 6 IK 7

RESULT 13

Q8RKN1

ID Q8RKN1 PRELIMINARY; PRT; 11 AA.
 AC Q8RKN1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Beta-lactamase CTX-M-9 (Fragment).
 GN BLACTX-M-9.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=743-D;
 RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,
 RA Prats G.;
 RT "A novel complex sull-type integron in Escherichia coli carrying the
 RT bla(CTX-M-9) gene.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY092058; AAM15718.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1071 MW; C26BF418D050440D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
 ||
 Db 1 AS 2

RESULT 14

Q9L4F7

ID Q9L4F7 PRELIMINARY; PRT; 11 AA.

AC Q9L4F7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Phosphatidylinositol-specific phospholipase C (PI-PLC)
 DE (Fragment).
 GN PLCA.
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14579 type strain;
 RX MEDLINE=20055637; PubMed=10589720;
 RA Okstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;
 RT "Sequence analysis of three Bacillus cereus loci under P*l*cR-regulated
 RT genes encoding degradative enzymes and enterotoxin."
 RL Microbiology 145:3129-3138(1999).
 DR EMBL; AJ243711; CAB69804.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KK 4
 ||
 Db 4 KK 5

RESULT 15

P77404
 ID P77404 PRELIMINARY; PRT; 11 AA.
 AC P77404;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE DNA sequence downstream of the ECOPRRI HSD locus (Fragment).
 GN HSDR.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97206151; PubMed=9157244;
 RA Tyndall C., Lehnherr H., Sandmeier U., Kulik E., Bickle T.A.;
 RT "The type IC hsd loci of the enterobacteria are flanked by DNA with
 RT high homology to the phage P*l* genome: implications for the evolution
 RT and spread of DNA restriction systems."
 RL Mol. Microbiol. 23:729-736(1997).
 DR EMBL; X98145; CAA66840.1; -.
 DR EMBL; X98144; CAA66839.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1259 MW; 714AB092A4072734 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KA 11
||
Db 10 KA 11

RESULT 16

Q9RQ60

ID Q9RQ60 PRELIMINARY; PRT; 11 AA.
AC Q9RQ60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Acetohydroxy acid synthase small subunit (Fragment).
GN ILVH.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022990; PubMed=10555290;
RA Clark M.A., Moran N.A., Baumann P.;
RT "Sequence evolution in bacterial endosymbionts having extreme base
RT compositions.";
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL; AF129503; AAF13796.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1330 MW; 0E89EF1E2045B050 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
||
Db 2 KR 3

RESULT 17

P71228

ID P71228 PRELIMINARY; PRT; 11 AA.
AC P71228;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nitrate/nitrite sensor transmitter (Fragment).
GN NARQ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=K-12;
 RX MEDLINE=92374842; PubMed=1508040;
 RA Chiang R.C., Cavicchioli R., Gunsalus R.P.;
 RT "Identification and characterization of narQ, a second nitrate sensor
 RT for nitrate-dependent gene regulation in Escherichia coli.";
 RL Mol. Microbiol. 6:1913-1923(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=97113461; PubMed=8955321;
 RA Cavicchioli R., Kolesnikow T., Chiang R.C., Gunsalus R.P.;
 RT "Characterization of the aegA locus of Escherichia coli: control of
 RT gene expression in response to anaerobiosis and nitrate.";
 RL J. Bacteriol. 178:6968-6974(1996).
 DR EMBL; L34011; AAB46943.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1200 MW; 52E1CFFCA2D77403 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
 ||
 Db 9 AS 10

RESULT 18
 Q93MI7

ID Q93MI7 PRELIMINARY; PRT; 11 AA.
 AC Q93MI7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Adhesin (Fragment).
 GN IHA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CFT073;
 RA Stell A.L.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF401752; AAK94916.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1203 MW; 8E2817ECBDD731B1 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
 ||
 Db 7 AS 8

RESULT 19

Q9RFZ2

ID Q9RFZ2 PRELIMINARY; PRT; 11 AA.
 AC Q9RFZ2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Fructose biphosphate aldolase (Fragment).
 GN FBA.
 OS Mycoplasma mycoides subsp. capri.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=40477;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG3;
 RX MEDLINE=20193983; PubMed=10727835;
 RA Thiaucourt F., Lorenzon S., David A., Breard A.;
 RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
 RT of a putative membrane protein gene."
 RL Vet. Microbiol. 72:251-268(2000).
 DR EMBL; AF162998; AAF15255.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1371 MW; 50B0881A3331FB57 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
 ||
 Db 2 PK 3

RESULT 20

P95518

ID P95518 PRELIMINARY; PRT; 11 AA.
 AC P95518;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein RpsA (Fragment).
 GN RPSA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHL101;
 RX MEDLINE=97164347; PubMed=9011038;
 RA Highlander S.K., Garza O., Brown B.J., Koby S., Oppenheim A.B.;
 RT "Isolation and characterization of the integration host factor genes
 RT of Pasteurella haemolytica."
 RL FEMS Microbiol. Lett. 146:181-188(1997).
 DR EMBL; U56139; AAC44845.1; -.
 FT NON_TER 1 1

SQ SEQUENCE 11 AA; 1168 MW; 7A4BFD38D339CDDDB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KA 11

||

Db 7 KA 8

RESULT 21

Q47345

ID Q47345 PRELIMINARY; PRT; 11 AA.
AC Q47345;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Leader peptide.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Faber F., van Giezen M., Van Gorcom R.F.M., Harder W.;
RT "Identification of two Escherichia coli K12 proteins which are induced
RT in response to pollutant stress.";
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 2-11 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=85134883; PubMed=6396419;
RA Hudson G.S., Davidson B.E.;
RT "Nucleotide sequence and transcription of the phenylalanine and
RT tyrosine operons of Escherichia coli K12.";
RL J. Mol. Biol. 180:1023-1051(1984).
DR EMBL; Z70523; CAA94435.1; -.
SQ SEQUENCE 11 AA; 1402 MW; 87AB199204141775 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7

||

Db 10 KR 11

RESULT 22

Q9AIZ8

ID Q9AIZ8 PRELIMINARY; PRT; 11 AA.
AC Q9AIZ8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
RA Baumann P.;
RT "Cospeciation of psyllids and their primary prokaryotic
RT endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861(2001).
DR EMBL; AF211126; AAK15376.1; -.
DR GO; GO:0004812; F:tRNA ligase activity; IEA.
KW Aminoacyl-tRNA synthetase.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1384 MW; 07A038324339C724 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
||
Db 1 NI 2

RESULT 23

Q44090

ID Q44090 PRELIMINARY; PRT; 11 AA.
AC Q44090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical export segment (Fragment).
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A-EF22;
RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;
RT "Sequence regions from Acholeplasma laidlawii which restore export of
RT beta-lactamase in Escherichia coli.";
RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z22875; CAA80495.1; -.
DR PIR; S33519; S33519.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KK 4
||
Db 2 KK 3

RESULT 24

Q44237

ID Q44237 PRELIMINARY; PRT; 11 AA.
AC Q44237;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glutamine synthetase (Fragment).
GN GLNA.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7120;
RA Warner L.E., Ligon P.J., Stahel A.W., Curtis S.E.;
RT "The apcF gene of Anabaena sp. strain PCC 7120 is regulated by
RT nitrogen and the apcF and glnA promoters overlap."
RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7120;
RA Scappino L.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U21853; AAA65652.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1316 MW; 2000580E32CB06C7 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
||
Db 9 KR 10

RESULT 25

Q9R872

ID Q9R872 PRELIMINARY; PRT; 11 AA.
AC Q9R872;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dihydrofolate reductase (Fragment).
GN DFR1.
OS Escherichia coli.

OG Plasmid r483.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RA Hansson K., Sundstrom L., Pelletier A., Roy P.H.;
 RT "Sequence and function of the second type of integron in Tn7.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RX MEDLINE=82220022; PubMed=6283361;
 RA Lichtenstein C., Brenner S.;
 RT "Unique insertion site of Tn7 in the E. coli chromosome.";
 RL Nature 297:601-603(1982).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RX MEDLINE=83290694; PubMed=6411680;
 RA Simonsen C.C., Chen E.Y., Levinson A.D.;
 RT "Identification of the type I trimethoprim-resistant dihydrofolate
 RT reductase specified by the Escherichia coli R-plasmid R483: Comparison
 RT with procaryotic and eucaryotic dihydrofolate reductases.";
 RL J. Bacteriol. 155:1001-1008(1983).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RX MEDLINE=83272957; PubMed=6308574;
 RA Fling M.E., Richards C.;
 RT "The nucleotide sequence of the trimethoprim-resistant dihydrofolate
 RT reductase gene harbored by Tn7.";
 RL Nucleic Acids Res. 11:5147-5158(1983).
 DR EMBL; AJ001816; CAA05032.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1221 MW; 92014864C2C69735 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
 ||
 Db 10 SK 11

RESULT 26

Q9R446

ID Q9R446 PRELIMINARY; PRT; 11 AA.
 AC Q9R446;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Carbamoyl-phosphate synthase subunit A (Fragment).

GN CARA.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11, and FA1090;
 RX MEDLINE=95291461; PubMed=7773412;
 RA Lawson F.S., Billowes F.M., Dillon J.A.;
 RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
 RT gonorrhoeae includes a large, variable intergenic sequence which is
 RT also present in other Neisseria species."
 RL Microbiology 141:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11, and FA1090;
 RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
 RT "Complexity of the variable sequence between the carbamoyl-phosphate
 RT synthase genes of Neisseria species."
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF029363; AAC78453.1; -.
 DR EMBL; AF029362; AAC78452.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DDD33694 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KA 11
 ||
 Db 6 KA 7

RESULT 27

Q8GMU3

ID Q8GMU3 PRELIMINARY; PRT; 11 AA.
 AC Q8GMU3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative catalase isozyme (Fragment).
 GN KATA.
 OS Acinetobacter lwoffii.
 OG Plasmid pKLH202.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=28090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TC108;
 RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
 RA Nikiforov V.G.;
 RT "pKLH2-like aberrant transposons and possible mechanisms of their
 RT dissemination."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ250245; CAC80800.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1233 MW; 81A15757B333276A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
||
Db 5 PK 6

RESULT 28

Q8GL24

ID Q8GL24 PRELIMINARY; PRT; 11 AA.
AC Q8GL24;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS *Borrelia burgdorferi* (Lyme disease spirochete).
OG Plasmid group cp32-6.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of *Borrelia burgdorferi* erp genes and their cp32
RT prophages: conservation amidst diversity."
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY142093; AAN17876.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1366 MW; 4E441D5330504373 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IK 10
||
Db 3 IK 4

RESULT 29

Q8GL19

ID Q8GL19 PRELIMINARY; PRT; 11 AA.
AC Q8GL19;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE PF-50 protein (Fragment).
 GN PF-50.
 OS *Borrelia burgdorferi* (Lyme disease spirochete).
 OG Plasmid group cp32-11.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sh-2-82;
 RA Stevenson B., Miller J.C.;
 RT "Comparative analyses of *Borrelia burgdorferi* erp genes and their cp32
 RT prophages: conservation amidst diversity."
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY142096; AAN17880.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1366 MW; 4E441D5337204373 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IK 10
 ||
 Db 3 IK 4

RESULT 30

Q7X566

ID Q7X566 PRELIMINARY; PRT; 11 AA.
 AC Q7X566;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS *Thermus thermophilus*.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC *Thermus*.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miyazaki T., Miyazaki J., Nishiyama M., Yamane H.;
 RT "Characterization of a LysN, the 4th enzyme in lysine biosynthesis, in
 RT an extremely thermophilic bacterium, *Thermus thermophilus* HB27."
 RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB097117; BAC76940.1; -.
 KW Hypothetical protein.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1073 MW; 39792C1E75B72EB8 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
 ||

Db 8 PK 9

RESULT 31

O60761

ID O60761 PRELIMINARY; PRT; 11 AA.
AC O60761;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NPT-1 protein (Fragment).
GN NPT-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98207718; PubMed=9545579;
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,
RA Tatsumi S., Morita K., Takeda E.;
RT "Characterization of the 5' flanking region of the human NPT-1
RT Na⁺/phosphate cotransporter gene."
RL Biochim. Biophys. Acta 1396:267-272(1998).
DR EMBL; D83236; BAA25645.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KK 4
||
Db 10 KK 11

RESULT 32

O75811

ID O75811 PRELIMINARY; PRT; 11 AA.
AC O75811;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ErbB-3 R2 (Fragment).
GN C-ERBB-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovarian carcinoma;
RX MEDLINE=98345147; PubMed=9681822;
RA Lee H., Maihle N.J.;
RT "Isolation and characterization of four alternate c-erbB3 transcripts
RT expressed in ovarian carcinoma-derived cell lines and normal human

RT tissues.";
RL Oncogene 16:3243-3252(1998).
DR EMBL; U88358; AAC39858.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1017 MW; 21B236366EB72878 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
||
Db 8 PK 9

RESULT 33

Q9H4H5

ID Q9H4H5 PRELIMINARY; PRT; 11 AA.
AC Q9H4H5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE DJ661I20.2 (Novel helicase C-terminal domain and SNF2 N-terminal
domains containing protein) (Fragment).
GN DJ620E11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Skuce C.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL031669; CAC17164.2; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1420 MW; 5EB2C32A3326D053 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KK 4
||
Db 7 KK 8

RESULT 34

Q15997

ID Q15997 PRELIMINARY; PRT; 11 AA.
AC Q15997;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RARA protein (Fragment).
GN RARA.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93222087; PubMed=7682097;
 RA Dong S., Geng J.P., Tong J.H., Wu Y., Cai J.R., Sun G.L., Chen S.R.,
 RA Wang Z.Y., Larsen C.J., Berger R., et al;
 RT "Breakpoint clusters of the PML gene in acute promyelocytic leukemia:
 RT primary structure of the reciprocal products of the PML-RARA gene in a
 RT patient with t(15;17).";
 RL Genes Chromosomes Cancer 6:133-139(1993).
 DR EMBL; S57794; AAD13888.1; -.
 DR PIR; I54081; I54081.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1277 MW; 33C70E22CDDDC417 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
 Db 10 KR 11

RESULT 35

Q9UCP5

ID Q9UCP5 PRELIMINARY; PRT; 11 AA.
 AC Q9UCP5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE AggreCAN core protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92235266; PubMed=1569188;
 RA Sandy J.D., Flannery C.R., Neame P.J., Lohmander L.S.;
 RL J. Clin. Invest. 89:1512-1516(1992).
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR GO; GO:0001501; P:skeletal development; NAS.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1149 MW; 8FBFE8DFE72042D5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
 ||
 Db 10 KP 11

RESULT 36

Q9UBM2

ID Q9UBM2 PRELIMINARY; PRT; 11 AA.
 AC Q9UBM2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ETV6 protein (Fragment).
 GN ETV6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Montgomery K.T., Lau S.T., Renault B., Yoon S.J., Baens M.,
 RA Marynen P., Kucherlapati R.;
 RT "Towards the Complete Sequence of Chromosome 12.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Baens M., Peeters P., Guo C., Aerssens J., Marynen P.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U81830; AAB39862.1; -.
 DR EMBL; U45432; AAB17016.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1194 MW; 8267C587A6DDC771 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IK 10
 ||
 Db 10 IK 11

RESULT 37

Q9H3V7

ID Q9H3V7 PRELIMINARY; PRT; 11 AA.
 AC Q9H3V7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Aquaporin-4 (Fragment).
 GN AQP4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97008105; PubMed=8855281;
 RA Lu M., Lee M.D., Smith B.L., Jung J.S., Agre P., Verdijsk M.A.J.,
 RA Merckx G., Rijss J.P.L., Deen P.M.T.;

RT "The human AQP4 gene: definition of the locus encoding two water
 RT channel polypeptides in brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:10908-10912(1996).
 DR EMBL; U63613; AAG17964.1; -.
 DR GO; GO:0005372; F:water transporter activity; NAS.
 DR GO; GO:0006833; P:water transport; NAS.
 KW Porin.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1233 MW; 379D9CA311AEB737 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
 ||
 Db 10 NI 11

RESULT 38

Q8NI03

ID Q8NI03 PRELIMINARY; PRT; 11 AA.
 AC Q8NI03;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE 25 hydroxyvitamin d3 1-alpha hydroxylase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ebert R., Schneider D., Jovanovic M., Adamski J., Jakob F.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF500480; AAM21669.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1298 MW; 82C14E84CB533731 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
 ||
 Db 8 AS 9

RESULT 39

Q26092

ID Q26092 PRELIMINARY; PRT; 11 AA.
 AC Q26092;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Sea STAR histone H2B gene 5'region (Fragment).

OS Pisaster ochraceus (Sea star).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
 OC Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Pisaster.
 OX NCBI_TaxID=7612;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sperm;
 RA Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;
 RT "Organization and Unusual Expression of Histone Genes in the Sea Star
 Pisaster ochraceus.";
 RL J. Mol. Evol. 25:29-36(1987).
 DR EMBL; X05619; CAA29106.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
 ||
 Db 3 PK 4

RESULT 40

Q9NL65

ID Q9NL65 PRELIMINARY; PRT; 11 AA.
 AC Q9NL65;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE ASABF-delta (Fragment).
 GN ASABF-DELTA.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kato Y.;
 RT "Ascaris suum asabf-delta gene, exon 2.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB029815; BAA89496.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1187 MW; 8BADD0CD1EAB5861 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
 Db 9 KR 10

RESULT 41

Q9TWX6

ID Q9TWX6 PRELIMINARY; PRT; 11 AA.
 AC Q9TWX6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide
 DE (Fragment).
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92134256; PubMed=1734862;
 RA Touhara K., Prestwich G.D.;
 RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
 RT binding protein.";
 RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
 ||
 Db 4 AS 5

RESULT 42

Q8MPQ3

ID Q8MPQ3 PRELIMINARY; PRT; 11 AA.
 AC Q8MPQ3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein Y23H5A.8b.
 GN Y23H5A.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;

RA Dempsey S., Le T.T.;
 RT "The sequence of C. elegans cosmid Y23H5A."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF077541; AAM54173.1; -.
 DR WormPep; Y23H5A.8b; CE31097.
 KW Hypothetical protein.
 SQ SEQUENCE 11 AA; 1319 MW; 6920D63A21B77414 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
 Db 8 KR 9

RESULT 43

Q86D32

ID Q86D32 PRELIMINARY; PRT; 11 AA.
 AC Q86D32;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Histone H1 (Fragment).
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dm28c;
 RX MEDLINE=22557728; PubMed=12670512;
 RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
 RA Campbell D.A.;
 RT "Evidence for multiple hybrid groups in Trypanosoma cruzi."
 RL Int. J. Parasitol. 33:269-279(2003).
 DR EMBL; AF545075; AAP21903.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1114 MW; CCC1B31E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KK 4
 ||
 Db 9 KK 10

RESULT 44

Q86D31

ID Q86D31 PRELIMINARY; PRT; 11 AA.

AC Q86D31;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Histone H1 (Fragment).
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sylvio X10;
 RX MEDLINE=22557728; PubMed=12670512;
 RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
 RA Campbell D.A.;
 RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";
 RL Int. J. Parasitol. 33:269-279(2003).
 DR EMBL; AF545076; AAP21906.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1174 MW; CCD1B21E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KK 4
 ||
 Db 9 KK 10

RESULT 45

Q9TRR7

ID Q9TRR7 PRELIMINARY; PRT; 11 AA.
 AC Q9TRR7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Calcyclin-associated protein, CAP50=CA2+/phospholipid-binding protein
 DE L-13 fragment (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92250478; PubMed=1533622;
 RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
 RT "A calyculin-associated protein is a newly identified member of the
 RT Ca2+/phospholipid-binding proteins, annexin family.";
 RL J. Biol. Chem. 267:8919-8924(1992).
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1310 MW; 55580B0F5DDAA9C7 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IK 10
||
Db 10 IK 11

RESULT 46

Q9TTQ0

ID Q9TTQ0 PRELIMINARY; PRT; 11 AA.
AC Q9TTQ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alanine glyoxylate aminotransferase (EC 2.6.1.44) (Fragment).
GN AGT.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20188798; PubMed=10723739;
RA Holbrook J.D., Birdsey G.M., Yang Z., Bruford M.W., Danpure C.J.;
RT "Molecular adaptation of alanine Glyoxylate aminotransferase targeting
RT in primates.";
RL Mol. Biol. Evol. 17:387-400(2000).
DR EMBL; AJ237887; CAB56788.1; -.
DR GO; GO:0008453; F:alanine-glyoxylate transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Aminotransferase; Transferase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1193 MW; E9F82B8BC7272331 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 47

O77872

ID O77872 PRELIMINARY; PRT; 11 AA.
AC O77872;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 1 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF049981; AAC41320.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
 ||
 Db 8 KP 9

RESULT 48

O77880

ID O77880 PRELIMINARY; PRT; 11 AA.
 AC O77880;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 2 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF049989; AAC41328.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1346 MW; AB5F2D9822D2DB56 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
 Db 8 KR 9

RESULT 49

O77908

ID O77908 PRELIMINARY; PRT; 11 AA.
AC O77908;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 2 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050019; AAC41358.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1261 MW; 4346CE9A7EB69EB3 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
||
Db 3 SK 4

RESULT 50

O77873

ID O77873 PRELIMINARY; PRT; 11 AA.
AC O77873;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 1 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).

DR EMBL; AF049982; AAC41321.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 8 KP 9

RESULT 51

O77871

ID O77871 PRELIMINARY; PRT; 11 AA.
AC O77871;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 1 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF049980; AAC41319.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 8 KP 9

RESULT 52

O77907

ID O77907 PRELIMINARY; PRT; 11 AA.
AC O77907;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE MHC class II B locus 2 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci."
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050018; AAC41357.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1346 MW; AB5F2D9822D2DB56 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
 Db 8 KR 9

RESULT 53

O77897

ID O77897 PRELIMINARY; PRT; 11 AA.
 AC O77897;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci."
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050007; AAC41346.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1280 MW; BCD47D9822D2DB56 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
||
Db 8 KR 9

RESULT 54

Q7YP62

ID Q7YP62 PRELIMINARY; PRT; 11 AA.
AC Q7YP62;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class Ib antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., He X., Xu L., Zeng Y.;
RT "Partial genomic sequence of HLA-F gene."
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY328516; AAP94210.1; -.
FT NON TER 1 1
SQ SEQUENCE 11 AA; 1208 MW; 2E0B6C5CC5AB45B8 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RN 8
||
Db 1 RN 2

RESULT 55

Q8ME62

ID Q8ME62 PRELIMINARY; PRT; 11 AA.
AC Q8ME62;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
DE (Fragment).
GN RBCL.
OS Porphyra carolinensis.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxID=76158;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=75;
RA Teasdale B.W., West A., Taylor H., Klein A.S.;

RT "A Simple Restriction Fragment Length Polymorphism (RFLP) Assay To
 RT Discriminate Common Porphyra (Rhodophyta) Taxa From The Northwest
 RT Atlantic.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF414594; AAN03001.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1177 MW; D8DE49C4B771AB02 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
 ||
 Db 10 NI 11

RESULT 56

Q8MEL7

ID Q8MEL7 PRELIMINARY; PRT; 11 AA.
 AC Q8MEL7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Sida hookeriana.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Sida.
 OX NCBI_TaxID=108446;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384624; AAM50396.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
 Db 1 KR 2

RESULT 57

Q9G5Y0

ID Q9G5Y0 PRELIMINARY; PRT; 11 AA.
AC Q9G5Y0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Pseudotrapelus sinaitus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
OC Pseudotrapelus.
OX NCBI_TaxID=118229;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards."
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics."
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128507; AAG00758.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1374 MW; B05439FE336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
||
Db 2 SK 3

RESULT 58

Q8MEM2

ID Q8MEM2 PRELIMINARY; PRT; 11 AA.
AC Q8MEM2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Lagunaria patersonia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.
 OX NCBI_TaxID=183274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384616; AAM50388.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KR 7
 ||
 Db 1 KR 2

RESULT 59

Q8MES5

ID Q8MES5 PRELIMINARY; PRT; 11 AA.
 AC Q8MES5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Abelmoschus manihot.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.
 OX NCBI_TaxID=183220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384561; AAM50399.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KR 7

Db ||
 1 KR 2

RESULT 60

Q8MEP0

ID Q8MEP0 PRELIMINARY; PRT; 11 AA.
AC Q8MEP0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus peralbus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183256;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron."
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384598; AAM50370.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
Db 1 KR 2

RESULT 61

Q8MER8

ID Q8MER8 PRELIMINARY; PRT; 11 AA.
AC Q8MER8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Dombeya tiliacea.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Dombeyoideae; Dombeya.
OX NCBI_TaxID=121875;
RN [1]

RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384569; AAM50407.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1424 MW; 7227C351D32AE9D4 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 KR 7
 ||
 Db 1 KR 2

RESULT 62

Q32704
 ID Q32704 PRELIMINARY; PRT; 11 AA.
 AC Q32704;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE NdhE protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bright yellow 4; TISSUE=Leaf;
 RX MEDLINE=88210537; PubMed=3329576;
 RA Hayashida N., Matsubayashi T., Shinozaki K., Sugiura M., Inoue K.,
 RA Hiyama T.;
 RT "The gene for the 9kd polypeptide, a possible apoprotein for the iron-
 RT sulfur centers A and B of the photosystem I complex in tobacco
 RT chloroplastDNA.";
 RL Curr. Genet. 12:247-250(1987).
 DR EMBL; X05881; CAA29303.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1338 MW; 008165EE304776CB CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 9 IK 10
 ||

Db 7 IK 8

RESULT 63

Q8MES1

ID Q8MES1 PRELIMINARY; PRT; 11 AA.
AC Q8MES1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Alyogyne pinoniana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
OX NCBI_TaxID=183226;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron."
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384566; AAM50404.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
||
Db 1 KR 2

RESULT 64

Q8MEP3

ID Q8MEP3 PRELIMINARY; PRT; 11 AA.
AC Q8MEP3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus normanii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183253;
RN [1]
RP SEQUENCE FROM N.A.

RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384595; AAM50367.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
 Db 1 KR 2

RESULT 65

Q8MEQ7

ID Q8MEQ7 PRELIMINARY; PRT; 11 AA.
 AC Q8MEQ7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus drummondii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384581; AAM50353.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
 Db 1 KR 2

RESULT 66

Q8MEL9

ID Q8MEL9 PRELIMINARY; PRT; 11 AA.
 AC Q8MEL9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Pavonia hastata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Pavonia.
 OX NCBI_TaxID=183278;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384622; AAM50394.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
 ||
 Db 1 KR 2

RESULT 67

Q8MER0

ID Q8MER0 PRELIMINARY; PRT; 11 AA.
 AC Q8MER0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus coatesii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183236;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";

RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384578; AAM50416.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KR 7
 ||
 Db 1 KR 2

RESULT 68

Q8MES3

ID Q8MES3 PRELIMINARY; PRT; 11 AA.
 AC Q8MES3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Alyogyne cravenii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
 OX NCBI_TaxID=183223;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384563; AAM50401.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KR 7
 ||
 Db 1 KR 2

RESULT 69

Q8MEP5

ID Q8MEP5 PRELIMINARY; PRT; 11 AA.

AC Q8MEP5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus microchlaenus.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183251;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384593; AAM50365.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 KR 7
 ||
 Db 1 KR 2

RESULT 70

Q8MER1
 ID Q8MER1 PRELIMINARY; PRT; 11 AA.
 AC Q8MER1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus calyphyllus.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183235;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384577; AAM50415.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
||
Db 1 KR 2

RESULT 71

Q8SKP8

ID Q8SKP8 PRELIMINARY; PRT; 11 AA.
AC Q8SKP8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Ctenophorus caudicinctus (Ring-tailed dragon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC Ctenophorus.
OX NCBI_TaxID=180905;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21623804; PubMed=11754013;
RA Melville J., Schulte J.A. II, Larson A.;
RT "A molecular phylogenetic study of ecological diversification in the
RT Australian lizard genus Ctenophorus."
RL J. Exp. Zool. 291:339-353(2001).
DR EMBL; AF375623; AAL78791.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1354 MW; A8F7371E33640336 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KR 7
||
Db 5 KR 6

RESULT 72

Q8MER7

ID Q8MER7 PRELIMINARY; PRT; 11 AA.
AC Q8MER7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Fioria vitifolia.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Fioria.
 OX NCBI_TaxID=183231;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384570; AAM50408.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 KR 7
 ||
 Db 1 KR 2

RESULT 73

Q8HGX5
 ID Q8HGX5 PRELIMINARY; PRT; 11 AA.
 AC Q8HGX5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribulose 1,5 biphosphate carboxylase large subunit (EC 4.1.1.39)
 DE (Fragment).
 GN RBCL.
 OS Rhabdothamnopsis sinensis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
 OC Rhabdothamnopsis.
 OX NCBI_TaxID=199121;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mayer V.E., Moeller M., Perret M., Weber A.;
 RT "Phylogenetic position and generic differentiation of Epithemateae
 RT (Gesneriaceae) inferred from cpDNA sequence data."
 RL Am. J. Bot. 0:0-0(0).
 DR EMBL; AJ490915; CAD36598.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.

DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
KW Lyase; Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1178 MW; C2833DEA21AB01B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 9 AS 10

RESULT 74

Q7Y9H0

ID Q7Y9H0 PRELIMINARY; PRT; 11 AA.
AC Q7Y9H0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Hypsilurus modestus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC Hypsilurus.
OX NCBI_TaxID=206594;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22653719; PubMed=12769459;
RA Schulte J.A. II, Melville J., Larson A.;
RT "Molecular phylogenetic evidence for ancient divergence of lizard taxa
RT on either side of Wallace's Line."
RL Proc. R. Soc. Lond., B, Biol. Sci. 270:597-603(2003).
DR EMBL; AY133015; AAN15868.1; -.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1335 MW; 0005371E33640440 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
||
Db 3 NI 4

RESULT 75

Q37925

ID Q37925 PRELIMINARY; PRT; 11 AA.
AC Q37925;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Bacteriophage fr replicase (Fragment).
 OS Bacteriophage fr.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Levivirus.
 OX NCBI_TaxID=12017;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Berzin V.M., Griбанov V.A., Cielens I.E., Jansone I.V., Gren E.J.;
 RT "The nucleotide sequence of the regulatory region of phage fr
 replicase cistron."
 RL Bioorg. Khim. 7:306-308(1981).
 DR EMBL; M34834; AAA32193.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1285 MW; 8BD43470C33321B1 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
 ||
 Db 2 SK 3

Search completed: April 8, 2004, 15:46:00
 Job time : 29.7692 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds
 (without alignments)
 111.135 Million cell updates/sec

Title: US-09-787-443A-1
 Perfect score: 11
 Sequence: 1 ASKKPKRNIKA 11

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Match	Length	DB	ID	Description
	Score	%					
1	4	36.4	11	1	CSI5_BACSU	P81095 bacillus su	
2	2	18.2	11	1	BPPB_AGKHA	P01021 agkistrodon	
3	2	18.2	11	1	BRK_MEGFL	P12797 megascolia	
4	2	18.2	11	1	EFG_CLOPA	P81350 clostridium	
5	2	18.2	11	1	LADD_ONCMY	P81018 oncorhynchu	
6	2	18.2	11	1	MORN_HUMAN	P01163 homo sapien	
7	2	18.2	11	1	OAIF_SARBU	P83518 sarcophaga	
8	2	18.2	11	1	PVK1_PERAM	P41837 periplaneta	
9	2	18.2	11	1	Q2OA_COMTE	P80464 comamonas t	
10	2	18.2	11	1	RR2_CONAM	P42341 conopholis	
11	2	18.2	11	1	TKN2_UPERU	P08616 uperoleia r	
12	2	18.2	11	1	TKNA_GADMO	P28498 gadus morhu	
13	2	18.2	11	1	TKNA_HORSE	P01290 equus cabal	
14	2	18.2	11	1	TKNA_ONCMY	P28499 oncorhynchu	
15	2	18.2	11	1	TKNA_RANCA	P22688 rana catesb	
16	2	18.2	11	1	TKNA_RANRI	P29207 rana ridibu	
17	2	18.2	11	1	TKNA_SCYCA	P41333 scyliorhinu	

18	2	18.2	11	1	TKND_RANCA	P22691	rana catesb
19	2	18.2	11	1	TKN_ELEMO	P01293	eledone mos
20	1	9.1	11	1	ANGT_CRIGE	P09037	crinia geor
21	1	9.1	11	1	ASL1_BACSE	P83146	bacteroides
22	1	9.1	11	1	ASL2_BACSE	P83147	bacteroides
23	1	9.1	11	1	BPP3_BOTIN	P30423	bothrops in
24	1	9.1	11	1	BPP4_BOTIN	P30424	bothrops in
25	1	9.1	11	1	BPP_AGKHP	P04562	agkistrodon
26	1	9.1	11	1	CA21_LITCI	P82087	litoria cit
27	1	9.1	11	1	CA22_LITCI	P82088	litoria cit
28	1	9.1	11	1	CA41_LITCI	P82091	litoria cit
29	1	9.1	11	1	CA42_LITCI	P82092	litoria cit
30	1	9.1	11	1	CEP1_ACHFU	P22790	achatina fu
31	1	9.1	11	1	CORZ_PERAM	P11496	periplaneta
32	1	9.1	11	1	COXA_CANFA	P99501	canis famil
33	1	9.1	11	1	CX5A_CONAL	P58848	conus aulic
34	1	9.1	11	1	CX5B_CONAL	P58849	conus aulic
35	1	9.1	11	1	CXL1_CONMR	P58807	conus marmo
36	1	9.1	11	1	ES1_RAT	P56571	rattus norv
37	1	9.1	11	1	FAR6_PENMO	P83321	penaeus mon
38	1	9.1	11	1	FAR9_CALVO	P41864	calliphora
39	1	9.1	11	1	HS70_PINPS	P81672	pinus pinas
40	1	9.1	11	1	LPW_THETH	P05624	thermus the
41	1	9.1	11	1	LSK1_LEUMA	P04428	leucophaea
42	1	9.1	11	1	LSKP_PERAM	P36885	periplaneta
43	1	9.1	11	1	MHBI_KLEPN	P80580	klebsiella
44	1	9.1	11	1	MLG_THETS	P41989	theromyzon
45	1	9.1	11	1	NUHM_CANFA	P49820	canis famil
46	1	9.1	11	1	NXSN_PSETE	P59072	pseudonaja
47	1	9.1	11	1	PKC1_CARMO	P82684	carausius m
48	1	9.1	11	1	PQQC_PSEFL	P55173	pseudomonas
49	1	9.1	11	1	RANC_RANPI	P08951	rana pipien
50	1	9.1	11	1	RE41_LITRU	P82074	litoria rub
51	1	9.1	11	1	RRPL_CHAV	P13179	chandipura
52	1	9.1	11	1	RS30_ONCMY	P83328	oncorhynch
53	1	9.1	11	1	T2P1_PROVU	P31031	proteus vul
54	1	9.1	11	1	TIN1_HOPTI	P82651	hoplobatrac
55	1	9.1	11	1	TIN4_HOPTI	P82654	hoplobatrac
56	1	9.1	11	1	TKC2_CALVO	P41518	calliphora
57	1	9.1	11	1	TKN1_PSEGU	P42986	pseudophryn
58	1	9.1	11	1	TKN1_UPEIN	P82026	uperoleia i
59	1	9.1	11	1	TKN1_UPERU	P08612	uperoleia r
60	1	9.1	11	1	TKN2_PSEGU	P42987	pseudophryn
61	1	9.1	11	1	TKN3_PSEGU	P42988	pseudophryn
62	1	9.1	11	1	TKN4_PSEGU	P42989	pseudophryn
63	1	9.1	11	1	TKN5_PSEGU	P42990	pseudophryn
64	1	9.1	11	1	TKNA_CHICK	P19850	gallus gall
65	1	9.1	11	1	TKN_PHYFU	P08615	physalaemus
66	1	9.1	11	1	UF05_MOUSE	P38643	mus musculu
67	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapien
68	1	9.1	11	1	UXB2_YEAST	P99013	saccharomyc
69	0	0.0	11	1	CA31_LITCI	P82089	litoria cit
70	0	0.0	11	1	CA32_LITCI	P82090	litoria cit

ALIGNMENTS

RESULT 1

CSI5_BACSU

ID CSI5_BACSU STANDARD; PRT; 11 AA.
 AC P81095;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=168 / JH642;
 RA Graumann P.L., Schmid R., Marahiel M.A.;
 RL Submitted (OCT-1997) to Swiss-Prot.
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=168 / JH642;
 RX MEDLINE=96345629; PubMed=8755892;
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
 RT "Cold shock stress-induced proteins in Bacillus subtilis."
 RL J. Bacteriol. 178:4611-4619(1996).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: In response to low temperature.
 CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RNIK 10
 ||||
 Db 2 RNIK 5

RESULT 2

BPPB_AGKHA

ID BPPB_AGKHA STANDARD; PRT; 11 AA.
 AC P01021;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide B (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=242054;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Kato H., Suzuki T.;

RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
 RT the venom of Agkistrodon halys blomhoffii.";
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01254; XASNBA.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
 ||
 Db 7 PK 8

RESULT 3

BRK_MEGFL

ID BRK_MEGFL STANDARD; PRT; 11 AA.
 AC P12797;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
 DE peptide ([Thr6]bradykinin)].
 OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Scoliidae; Megascolia.
 OX NCBI_TaxID=7437;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 RT solitary wasp Megascolia flavifrons.";
 RL Toxicon 25:527-535(1987).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Nakajima T., Piek T., Yashuara T., Mantel P.;
 RT "Two kinins isolated from the venom of Megascolia flavifrons.";
 RL Toxicon 26:34-34(1988).
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 DR PIR; B26744; B26744.
 DR GO; GO:0005615; C:extracellular space; IDA.
 DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.

KW Bradykinin; Vasodilator.

FT PEPTIDE 1 11 MEGASCOLIAKININ.

FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.

SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KA 11

||

Db 10 KA 11

RESULT 4

EFG_CLOPA

ID EFG_CLOPA STANDARD; PRT; 11 AA.

AC P81350;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Elongation factor G (EF-G) (CP 5) (Fragment).

GN FUSA.

OS Clostridium pasteurianum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1501;

RN [1]

RP SEQUENCE.

RC STRAIN=W5;

RX MEDLINE=98291870; PubMed=9629918;

RA Flengsrud R., Skjeldal L.;

RT "Two-dimensional gel electrophoresis separation and N-terminal

RT sequence analysis of proteins from Clostridium pasteurianum W5.";

RL Electrophoresis 19:802-806(1998).

CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.

CC EF-G/EF-2 subfamily.

DR InterPro; IPR000795; EF_GTPbind.

DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.

KW Elongation factor; Protein biosynthesis; GTP-binding.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9

||

Db 9 NI 10

RESULT 5

LADD_ONCMY

ID LADD_ONCMY STANDARD; PRT; 11 AA.
 AC P81018;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Ladderlectin (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Blood;
 RX MEDLINE=97293418; PubMed=9149391;
 RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;
 RT "A rainbow trout lectin with multimeric structure."
 RL Comp. Biochem. Physiol. 116B:385-390(1997).
 CC -!- FUNCTION: Lectin that binds sepharose.
 CC -!- COFACTOR: Calcium is essential for sepharose binding.
 CC -!- SUBUNIT: Multimeric.
 KW Lectin; Calcium.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RN 8
 ||
 Db 5 RN 6

RESULT 6

MORN_HUMAN

ID MORN_HUMAN STANDARD; PRT; 11 AA.
 AC P01163;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Morphogenetic neuropeptide (Head activator) (HA).
 OS Homo sapiens (Human),
 OS Rattus norvegicus (Rat),
 OS Bos taurus (Bovine),
 OS Anthopleura elegantissima (Sea anemone), and
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human, Rat, and Bovine;
 RX MEDLINE=82035850; PubMed=7290191;
 RA Bodenmuller H., Schaller H.C.;
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,

RT from coelenterates to humans.";
 RL Nature 293:579-580(1981).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=A.elegantissima, and H.attenuata;
 RA Schaller H.C., Bodenmuller H.;
 RT "Isolation and amino acid sequence of a morphogenetic peptide from
 RT hydra.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
 RN [3]
 RP SYNTHESIS.
 RX MEDLINE=82050803; PubMed=7297679;
 RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
 RT "Synthesis of a new neuropeptide, the head activator from hydra.";
 RL FEBS Lett. 131:317-321(1981).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=90059923; PubMed=2583101;
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
 RT in the G2/mitosis transition.";
 RL EMBO J. 8:3311-3318(1989).
 CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
 CC in the G2/mitosis transition.
 CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
 CC and was called head activator by the authors, because it induced
 CC head-specific growth and differentiation in this animal. It has
 CC been found in mammalian intestine and hypothalamus.
 DR PIR; A01427; YHRT.
 DR PIR; A93900; YHXA.E.
 DR PIR; B01427; YHHU.
 DR PIR; B93900; YHJFHY.
 DR PIR; C01427; YHBO.
 DR GK; P01163; -.
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
 ||
 Db 6 SK 7

RESULT 7

OAIF_SARBU
 ID OAIF_SARBU STANDARD; PRT; 11 AA.
 AC P83518;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-
 DE ODAIF(1-9); Neb-ODAIF(1-7)].
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RC TISSUE=Ovary;
 RX MEDLINE=22272747; PubMed=12383874;
 RA Vandingenen A., Hens K., Baggerman G., Macours N., Schoofs L.,
 RA De Loof A., Huybrechts R.;
 RT "Isolation and characterization of an angiotensin converting enzyme
 RT substrate from vitellogenic ovaries of *Neobellieria bullata*.";
 RL Peptides 23:1853-1863(2002).
 CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
 CC vitro.
 CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-
 CC terminal dipeptides.
 CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
 CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
 FT PEPTIDE 1 11 NEB-ODAIF.
 FT PEPTIDE 1 9 NEB-ODAIF(1-9).
 FT PEPTIDE 1 7 NEB-ODAIF(1-7).
 SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
 ||
 Db 4 KP 5

RESULT 8

PVK1_PERAM
 ID PVK1_PERAM STANDARD; PRT; 11 AA.
 AC P41837;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Periviscerokinin-1 (Pea-PVK-1).
 OS *Periplaneta americana* (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; *Periplaneta*.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Abdominal perisymphathetic organs;
 RX MEDLINE=95232021; PubMed=7716075;
 RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
 RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
 RT perisymphathetic organs of the American cockroach.";
 RL Peptides 16:61-66(1995).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
 CC HYPERNEURAL MUSCLE.
 KW Neuropeptide; Amidation.

FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 9

Q2OA_COMTE

ID Q2OA_COMTE STANDARD; PRT; 11 AA.
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)2-oxo-
CC 1,2-dihydroquinoline.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
CC step.
CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and
CC two gamma chains (Probable).
DR PIR; S66606; S66606.
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 9 KP 10

RESULT 10

RR2_CONAM
ID RR2_CONAM STANDARD; PRT; 11 AA.
AC P42341;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S2 (Fragment).
GN RPS2.
OS Conopholis americana (Squawroot).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.
OX NCBI_TaxID=4179;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92145776; PubMed=1723664;
RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
RT of photosynthesis in a lineage of parasitic plants."
RL Curr. Genet. 20:515-518(1991).
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; X64567; CAA45868.1; -.
DR PIR; S32575; S32575.
DR HAMAP; MF_00291; -; 1.
DR InterPro; IPR001865; Ribosomal_S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Ribosomal protein; Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NI 9
||
Db 7 NI 8

RESULT 11
TKN2_UPERU
ID TKN2_UPERU STANDARD; PRT; 11 AA.
AC P08616;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80223080; PubMed=7389029;
RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
RT "Physalaemin- and bombesin-like peptides in the skin of the
RT Australian leptodactylid frog Uperoleia rugosa.";
RL Chem. Pharm. Bull. 28:689-695(1980).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
||
Db 4 PK 5

RESULT 12

TKNA_GADMO
ID TKNA_GADMO STANDARD; PRT; 11 AA.
AC P28498;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;

RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23306; S23306.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
 ||
 Db 1 KP 2

RESULT 13

TKNA_HORSE

ID TKNA_HORSE STANDARD; PRT; 11 AA.
 AC P01290;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Equus caballus (Horse), and
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796, 10141;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Horse;
 RA Studer R.O., Trzeciak A., Lergier W.;
 RT "Isolation and amino-acid sequence of substance P from horse
 RT intestine.";
 RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.porcellus;
 RX MEDLINE=90044685; PubMed=2478925;
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P.";
 RL Neuropeptides 14:105-110(1989).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01558; SPHO.
 DR PIR; A60654; A60654.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PK 6
 ||
 Db 2 PK 3

RESULT 14

TKNA_ONCMY

ID TKNA_ONCMY STANDARD; PRT; 11 AA.
 AC P28499;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout."
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23308; S23308.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 1 KP 2

RESULT 15

TKNA_RANCA

ID TKNA_RANCA STANDARD; PRT; 11 AA.
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin A (RTK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A61033; A61033.
DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 1 KP 2

RESULT 16

TKNA_RANRI

ID TKNA_RANRI STANDARD; PRT; 11 AA.
AC P29207;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranakinin (Substance-P-related peptide).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda."
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
||
Db 1 KP 2

RESULT 17

TKNA_SCYCA

ID TKNA_SCYCA STANDARD; PRT; 11 AA.

AC P41333;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93292508; PubMed=7685693;
 RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
 RT "Primary structures and biological activities of substance-P-related
 RT peptides from the brain of the dogfish, Scyliorhinus canicula.";
 RL Eur. J. Biochem. 214:469-474(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S33300; S33300.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
 ||
 Db 1 KP 2

RESULT 18

TKND_RANCA

ID TKND_RANCA STANDARD; PRT; 11 AA.
 AC P22691;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin D (RTK D).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;

RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D61033; D61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KP 5
 ||
 Db 1 KP 2

RESULT 19

TKN_ELEMO

ID TKN_ELEMO STANDARD; PRT; 11 AA.
 AC P01293;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Eledoisin.
 OS Eledone moschata (Musky octopus) (*Ozaena moschata*), and
 OS Eledone cirrhosa (Curled octopus) (*Ozaena cirrosa*).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
 OX NCBI_TaxID=6641, 102876;
 RN [1]
 RP SEQUENCE.
 RA Anastasi A., Erspamer V.;
 RT "The isolation and amino acid sequence of eledoisin, the active
 RT endecapeptide of the posterior salivary glands of Eledone.";
 RL Arch. Biochem. Biophys. 101:56-65(1963).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01561; EEOC.
 DR PIR; B01561; EOCC.
 DR PDB; 1MXQ; 18-FEB-03.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
 KW 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SK 3
 ||
 Db 3 SK 4

RESULT 20

ANGT_CRIGE
 ID ANGT_CRIGE STANDARD; PRT; 11 AA.
 AC P09037;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Crinia-angiotensin II.
 OS Crinia georgiana (Quacking frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Crinia.
 OX NCBI_TaxID=8374;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80024575; PubMed=488254;
 RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endecapeptide from the skin of the Australian
 RT frog Crinia georgiana."
 RL Experientia 35:1132-1133(1979).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S07207; S07207.
 KW Vasoconstrictor.
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 1 A 1

RESULT 21

ASL1_BACSE

ID ASL1_BACSE STANDARD; PRT; 11 AA.
AC P83146;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15."
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 N 8
|
Db 1 N 1

RESULT 22

ASL2_BACSE

ID ASL2_BACSE STANDARD; PRT; 11 AA.
AC P83147;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;

RN [1]
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two
 RT novel heparinases, from *Bacteroides stercoris* HJ-15.";
 RL Eur. J. Biochem. 268:2635-2641(2001).
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
 CC heparin and heparan sulfate.
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-
 CC mercaptoethanol.
 CC -!- SUBUNIT: Monomer.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
 CC 7.2 and optimum temperature 45 degrees Celsius.
 KW Lyase; Heparin-binding.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 4 A 4

RESULT 23

BPP3_BOTIN

ID BPP3_BOTIN STANDARD; PRT; 11 AA.
 AC P30423;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from *Bothrops insularis* snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.

DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
|
Db 4 P 4

RESULT 24

BPP4_BOTIN

ID BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; D37196; D37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
|
Db 4 P 4

RESULT 25

BPP_AGKHP

ID BPP_AGKHP STANDARD; PRT; 11 AA.

AC P04562;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
 OS pallas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=8714;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=86177022; PubMed=3008123;
 RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
 RT "Structure-function studies on the bradykinin potentiating peptide
 RT from Chinese snake venom (Agkistrodon halys pallas).";
 RL Peptides 6 Suppl. 3:339-342(1985).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; JC0002; XAVIBH.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 R 7
 |
 Db 3 R 3

RESULT 26

CA21_LITCI

ID CA21_LITCI STANDARD; PRT; 11 AA.
 AC P82087;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 2.1/2.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue

RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 7 A 7

RESULT 27

CA22_LITCI

ID CA22_LITCI STANDARD; PRT; 11 AA.
 AC P82088;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 2.2/2.2Y4.
 OS *Litoria citropa* (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; *Litoria*.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 7 A 7

RESULT 28

CA41_LITCI

ID CA41_LITCI STANDARD; PRT; 11 AA.
 AC P82091;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.1/4.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
|
Db 7 S 7

RESULT 29

CA42_LITCI

ID CA42_LITCI STANDARD; PRT; 11 AA.

AC P82092;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein 4.2/4.2Y4.

OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

OC Pelodyadinae; Litoria.

OX NCBI_TaxID=94770;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RX MEDLINE=20057701; PubMed=10589099;

RA Wabnitz P.A., Bowie J.H., Tyler M.J.;

RT "Caerulein-like peptides from the skin glands of the Australian blue

RT montains tree frog Litoria citropa. Part 1. Sequence determination

RT using electrospray mass spectrometry.";

RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).

CC -!- FUNCTION: Hypotensive neuropeptide (Probable).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin dorsal glands.

CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being

CC sulfated.

CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; FALSE_NEG.

KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 4 4 SULFATION.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
|
Db 7 S 7

RESULT 30

CEP1_ACHFU

ID CEPl_ACHFU STANDARD; PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica."
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also
CC excitatory actions on the penis retractor muscle, the buccal
CC muscle and the identified neurons controlling the buccal muscle
CC movement of achatina.
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
|
Db 1 S 1

RESULT 31

CORZ_PERAM

ID CORZ_PERAM STANDARD; PRT; 11 AA.
AC P11496;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Corazonin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89325572; PubMed=2753132;
RA Veenstra J.A.;
RT "Isolation and structure of corazonin, a cardioactive peptide from
RT the American cockroach.";

RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
 CC in the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
 |
 Db 6 S 6

RESULT 32

COXA_CANFA

ID COXA_CANFA STANDARD; PRT; 11 AA.
 AC P99501;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
 GN COX5A.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins."
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c
 CC oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
 DR HSC-2DPAGE; P99501; DOG.
 DR InterPro; IPR003204; Cyt_c_ox5A.
 DR Pfam; PF02284; COX5A; 1.
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
|
Db 1 S 1

RESULT 33

CX5A_CONAL

ID CX5A_CONAL STANDARD; PRT; 11 AA.
AC P58848;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5a.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins."
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
CC observed when injected into mice.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
DR PIR; A59146; A59146.
KW Toxin.
FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
|
Db 4 P 4

RESULT 34

CX5B_CONAL

ID CX5B_CONAL STANDARD; PRT; 11 AA.

AC P58849;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Conotoxin au5b.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins."
 RL J. Biol. Chem. 274:30664-30671(1999).
 RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
 DR PIR; B59146; B59146.
 KW Toxin.
 FT DISULFID 2 9
 FT DISULFID 3 10
 SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
 |
 Db 4 P 4

RESULT 35

CXL1_CONMR

ID CXL1_CONMR STANDARD; PRT; 11 AA.

AC P58807;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Lambda-conotoxin CMrVIA.

OS Conus marmoreus (Marble cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the
 RT venom of *Conus marmoreus*.";
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 2 11
 FT DISULFID 3 8
 FT MOD RES 10 10 HYDROXYLATION.
 SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
 |
 Db 6 K 6

RESULT 36

ES1_RAT
 ID ES1 RAT STANDARD; PRT; 11 AA.
 AC P56571;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE ES1 protein, mitochondrial (Fragment).
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Rattus*.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
 CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot
 CC P2) is: 8.9, its MW is: 25 kDa.
 CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 R 7
|
Db 1 R 1

RESULT 37

FAR6_PENMO

ID FAR6_PENMO STANDARD; PRT; 11 AA.
AC P83321;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 R 7
|
Db 3 R 3

RESULT 38

FAR9_CALVO

ID FAR9_CALVO STANDARD; PRT; 11 AA.
AC P41864;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE CalliFMRFamide 9.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRFamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR; I41978; I41978.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 S 2
 |
 Db 1 S 1

RESULT 39

HS70 PINPS

ID HS70 PINPS STANDARD; PRT; 11 AA.
 AC P81672;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Heat shock 70 kDa protein (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
 CC (spot N164) is: 5.4, its MW is: 73 kDa.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 KW ATP-binding; Heat shock; Multigene family.

FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 I 9
|
Db 3 I 3

RESULT 40

LPW THETH

ID LPW THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT HB8 trpE and trpG."
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.

CC -----
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DR EMBL; X07744; CAA30565.1; -.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 41

LSK1_LEUMA

ID LSK1_LEUMA STANDARD; PRT; 11 AA.
 AC P04428;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Leucosulfakinin-I (LSK-I).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86315858; PubMed=3749893;
 RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
 RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
 RT gastrin and cholecystokinin."
 RL Science 234:71-73(1986).
 CC -!- FUNCTION: Change the frequency and amplitude of contractions of
 CC the hingat. Inhibits muscle contraction of hindgut.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR PIR; A01622; GMROL.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Hormone; Amidation; Sulfation.
 FT MOD_RES 6 6 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 R 7
 |
 Db 10 R 10

RESULT 42

LSKP_PERAM

ID LSKP_PERAM STANDARD; PRT; 11 AA.
 AC P36885;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Perisulfakinin (Pea-SK-I).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;

RX MEDLINE=90137190; PubMed=2615921;
 RA Veenstra J.A.;
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
 RT the American cockroach homologous to the leucosulfakinins.";
 RL Neuropeptides 14:145-149(1989).
 CC -!- FUNCTION: Stimulates hindgut contractions.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR PIR; A60656; A60656.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Hormone; Amidation; Sulfation.
 FT MOD_RES 6 6 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 R 7
 |
 Db 10 R 10

RESULT 43

MHBI_KLEPN
 ID MHBI_KLEPN STANDARD; PRT; 11 AA.
 AC P80580;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
 GN MHBI.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96349117; PubMed=8760924;
 RA Robson N.D., Parrott S., Cooper R.A.;
 RT "In vitro formation of a catabolic plasmid carrying Klebsiella
 RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
 RT hydroxybenzoate.";
 RL Microbiology 142:2115-2120(1996).
 CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
 KW Isomerase.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
 |
 Db 2 K 2

RESULT 44

MLG_THETS

ID MLG_THETS STANDARD; PRT; 11 AA.
 AC P41989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 OX NCBI_TaxID=13286;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94298944; PubMed=8026574;
 RA Salzet M., Wattez C., Bulet P., Malecha J.;
 RT "Isolation and structural characterization of a novel peptide related
 RT to gamma-melanocyte stimulating hormone from the brain of the leech
 RT Theromyzon tessulatum.";
 RL FEBS Lett. 348:102-106(1994).
 CC -!- SIMILARITY: Belongs to the POMC family.
 DR PIR; S45698; S45698.
 KW Hormone; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
 |
 Db 10 K 10

RESULT 45

NUHM_CANFA

ID NUHM_CANFA STANDARD; PRT; 11 AA.
 AC P49820;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Fragment).
 GN NDUFV2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;

RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
 CC FRAGMENT OF THE ENZYME.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
 CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
 CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
 CC mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
 DR HSC-2DPAGE; P49820; DOG.
 DR InterPro; IPR002023; Cmplx1_24kDa.
 DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
 KW Iron-sulfur; Iron; 2Fe-2S.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 2 A 2

RESULT 46

NXSN_PSETE
 ID NXSN_PSETE STANDARD; PRT; 11 AA.
 AC P59072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).
 OS Pseudonaja textilis (Eastern brown snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99449602; PubMed=10518793;
 RA Gong N.L., Armugam A., Jeyaseelan K.;
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
 RT cloning, expression and protein characterization.";
 RL Eur. J. Biochem. 265:982-989(1999).
 CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
 CC acetylcholine receptors (nAChR).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.

CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
 CC -!- SIMILARITY: Belongs to the snake toxin family.
 DR InterPro; IPR003571; Snake_toxin.
 DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
 KW Acetylcholine receptor inhibitor; Multigene family.
 FT UNSURE 3 3
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
 |
 Db 5 K 5

RESULT 47

PKC1_CARMO

ID PKC1_CARMO STANDARD; PRT; 11 AA.
 AC P82684;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).
 OS Carausius morosus (Indian stick insect).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
 OC Heteronemiidae; Carausius.
 OX NCBI_TaxID=7022;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RA Predel R., Kellner R., Gaede G.;
 RT "Myotropic neuropeptides from the retrocerebral complex of the stick
 RT insect, Carausius morosus (Phasmatodea: Lonchodidae).";
 RL Eur. J. Entomol. 96:275-278(1999).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
 |
 Db 9 P 9

RESULT 48

PQQC_PSEFL

ID PQQC_PSEFL STANDARD; PRT; 11 AA.
 AC P55173;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone
 DE biosynthesis protein C) (Fragment).
 GN PQQC.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHA0;
 RX MEDLINE=96064397; PubMed=8526497;
 RA Schnider U., Keel C., Defago G., Haas D.;
 RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:
 RT mutational inactivation of the genes results in overproduction of the
 RT antibiotic pyoluteorin.";
 RL Appl. Environ. Microbiol. 61:3856-3864(1995).
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -!- SIMILARITY: Belongs to the pqqC family.

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DR EMBL; X87299; CAA60734.1; -.
 DR PIR; S58244; S58244.
 DR HAMAP; MF_00654; -; 1.
 KW PQQ biosynthesis.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
 |
 Db 5 P 5

RESULT 49

RANC_RANPI

ID RANC_RANPI STANDARD; PRT; 11 AA.
 AC P08951;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatensin-C.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=84131098; PubMed=6141890;
 RA Nakajima T.;
 RL Unpublished results, cited by:
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
 RL Comp. Biochem. Physiol. 77C:99-108(1984).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
 CC family.
 DR InterPro; IPR000874; Bombesin.
 DR Pfam; PF02044; Bombesin; 1.
 DR PROSITE; PS00257; BOMBESIN; 1.
 KW Amphibian defense peptide; Bombesin family; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
 |
 Db 3 P 3

RESULT 50

RE41 LITRU
 ID RE41 LITRU STANDARD; PRT; 11 AA.
 AC P82074;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rubellidin 4.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians."
 RL Aust. J. Chem. 49:955-963(1996).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic

CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 I 9
 |
 Db 5 I 5

RESULT 51

RRPL_CHAV

ID RRPL_CHAV STANDARD; PRT; 11 AA.
 AC P13179;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
 DE (L protein) (Fragment).
 GN L.
 OS Chandipura virus (strain I653514).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Vesiculovirus.
 OX NCBI_TaxID=11273;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89299473; PubMed=2741347;
 RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
 RA Banerjee A.K.;
 RT "Structure and expression of the glycoprotein gene of Chandipura
 RT virus."
 RL Virology 171:285-290(1989).
 CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
 CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
 CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA} (N).
 CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
 CC NUCLEOCAPSID (N) PROTEIN.
 CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
 CC PARAMYXOVIRUSES.

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 CC -----

DR EMBL; J04350; AAA42917.1; -.
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 N 8
|
Db 4 N 4

RESULT 52

RS30_ONCMY

ID RS30_ONCMY STANDARD; PRT; 11 AA.
AC P83328;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S30 (Fragment).
GN FAU.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RX MEDLINE=22142142; PubMed=12147245;
RA Fernandes J.M.O., Smith V.J.;
RT "A novel antimicrobial function for a ribosomal peptide from rainbow
RT trout skin.";
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW Ribosomal protein; Antibiotic.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 53

T2P1_PROVU

ID T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;

DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
 DE (R.PvuI) (Fragment).
 GN PVUIR.
 OS *Proteus vulgaris*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Proteus*.
 OX NCBI_TaxID=585;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13315;
 RX MEDLINE=93087186; PubMed=1454536;
 RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
 RT "Cloning and characterization of genes for the PvuI restriction and
 RT modification system."
 RL Nucleic Acids Res. 20:5743-5747(1992).
 CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
 CC CLEAVES AFTER T-4.
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 CC specific double-stranded fragments with terminal 5'-phosphates.
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 CC -----
 DR EMBL; L04163; AAA25660.1; -.
 DR PIR; S35490; S35490.
 DR REBASE; 1541; PvuI.
 KW Restriction system; Hydrolase; Nuclease; Endonuclease.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 I 9
 |
 Db 1 I 1

RESULT 54

TIN1_HOPTI
 ID TIN1_HOPTI STANDARD; PRT; 11 AA.
 AC P82651;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tigerinin-1.
 OS *Hoplobatrachus tigerinus* (Indian bull frog) (*Rana tigerina*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog *Rana*
 RT *tigerina*.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against *B.subtilis*, *E.coli*,
 CC *S.aureus*, *M.luteus*, *P.putida* and *S.cerevisiae*.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
 FT DISULFID 2 10
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 9 I 9
 |
 Db 5 I 5

RESULT 55

TIN4_HOPTI
 ID TIN4_HOPTI STANDARD; PRT; 11 AA.
 AC P82654;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tigerinin-4.
 OS Hoplobatrachus tigerinus (Indian bull frog) (*Rana tigerina*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog *Rana*
 RT *tigerina*.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against *B.subtilis*, *E.coli*,
 CC *S.aureus*, *M.luteus*, *P.putida* and *S.cerevisiae*.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.

CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 R 7
|
Db 1 R 1

RESULT 56

TKC2_CALVO

ID TKC2_CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: Myoactive peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 N 8
|
Db 4 N 4

RESULT 57

TKN1_PSEGU

ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-I (PG-KI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; B60409; B60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
 |
 Db 2 P 2

RESULT 58
 TKN1_UPEIN
 ID TKN1_UPEIN STANDARD; PRT; 11 AA.
 AC P82026;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperin 1.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.

OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 2 A 2

RESULT 59

TKN1 UPERU
 ID TKN1 UPERU STANDARD; PRT; 11 AA.
 AC P08612;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperolein.
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspamer V., Endean R.;
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
 RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
 |
 Db 2 P 2

RESULT 60

TKN2_PSEGU

ID TKN2_PSEGU STANDARD; PRT; 11 AA.
 AC P42987;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-II (PG-KII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; C60409; C60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.

DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
 |
 Db 2 P 2

RESULT 61

TKN3_PSEGU

ID TKN3_PSEGU STANDARD; PRT; 11 AA.
 AC P42988;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-III (PG-KIII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D60409; D60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
|
Db 2 P 2

RESULT 62

TKN4_PSEGU

ID TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409; E60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
|
Db 2 P 2

RESULT 63

TKN5_PSEGU

ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
|
Db 2 P 2

RESULT 64

TKNA_CHICK

ID TKN_A_CHICK STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=88204263; PubMed=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine."
 RL Regul. Pept. 20:171-180(1988).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; JN0023; JN0023.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 R 7
 |
 Db 1 R 1

RESULT 65

TKN_PHYFU

ID TKN_PHYFU STANDARD; PRT; 11 AA.
 AC P08615;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Physalaemin.
 OS Physalaemus fuscumaculatus (Neotropical frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
 OC Leptodactylinae; Physalaemus.
 OX NCBI_TaxID=8378;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;

RX MEDLINE=66076612; PubMed=5857249;
 RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
 RT "Structure and pharmacological actions of physalaemin, the main
 RT active polypeptide of the skin of *Physalaemus fuscumaculatus*.";
 RL Experientia 20:489-490(1964).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07201; S07201.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 2 A 2

RESULT 66

UF05_MOUSE

ID UF05_MOUSE STANDARD; PRT; 11 AA.
 AC P38643;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familiar and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis."
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 48 kDa.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFa CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 67

ULAG_HUMAN

ID ULAG_HUMAN STANDARD; PRT; 11 AA.
AC P31933;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993."
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 34 kDa.
DR SWISS-2DPAGE; P31933; HUMAN.
DR Siena-2DPAGE; P31933; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 6 A 6

RESULT 68

UXB2_YEAST

ID UXB2_YEAST STANDARD; PRT; 11 AA.
AC P99013;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]

RP SEQUENCE.
 RC STRAIN=X2180-1A;
 RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,
 RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
 RL Submitted (AUG-1995) to Swiss-Prot.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.20, its MW is: 9.2 kDa.
 DR SWISS-2DPAGE; P99013; YEAST.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 7 A 7

RESULT 69

CA31_LITCI

ID CA31_LITCI STANDARD; PRT; 11 AA.
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 0.0%; Score 0; DB 1; Length 11;
Best Local Similarity 0.0%; Pred. No. 1.4e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1

Db 1 Q 1

RESULT 70

CA32_LITCI

ID CA32_LITCI STANDARD; PRT; 11 AA.

AC P82090;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein 3.2/3.2Y4.

OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

OC Pelodyadinae; Litoria.

OX NCBI_TaxID=94770;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RX MEDLINE=20057701; PubMed=10589099;

RA Wabnitz P.A., Bowie J.H., Tyler M.J.;

RT "Caerulein-like peptides from the skin glands of the Australian blue

RT montains tree frog Litoria citropa. Part 1. Sequence determination

RT using electrospray mass spectrometry.";

RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).

CC -!- FUNCTION: Hypotensive neuropeptide (Probable).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin dorsal glands.

CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
sulfated.

CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; FALSE_NEG.

KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 4 4 SULFATION.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 0.0%; Score 0; DB 1; Length 11;
Best Local Similarity 0.0%; Pred. No. 1.4e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1

Db 1 Q 1

Search completed: April 8, 2004, 15:47:18
Job time : 6.15385 secs